

(TM)

ch nn n.a. - n.a. database search, using Smith-Waterman algorithm

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Title:
Description:
>US-08-963-656-1
(1-1689) from US08963656.seq
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Scoring table: TABLE default

Searched: 567134 seqs, 1101898692 bases x 2

Database: emb155

genbank107

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score		Query Match	Length	DB	ID	Description	Pred. No.
	Score	Match						
1	1686	99.9	1689	25	HSU49727	Human C-C chemokine re	0.00e+00	
2	1637	97.0	1717	25	HSU51241	Human eosinophil eotax	0.00e+00	
3	1193	70.1	1201	27	HSU28694	Human eosinophil CC ch	0.00e+00	
4	1064	63.0	1068	26	AF026535	Homo sapiens chemokine	0.00e+00	
5	958	56.8	1068	26	CAY13775	Cercopithecus aethiops	0.00e+00	
6	932	56.4	1068	26	MW13776	Macaca mulatta CCR-3 g	0.00e+00	
7	948	56.2	1068	26	AFU17283	Macaca mulatta chemoki	0.00e+00	
8	600	35.5	1440	28	MW28406	Mus musculus macrophag	0.00e+00	
9	570	33.8	1185	28	MW26677	Mus musculus chemokine	0.00e+00	
10	558	33.1	1315	28	RNP0K93	Rattus norvegicus mRNA	0.00e+00	
11	551	32.6	1080	28	AF003954	Rattus norvegicus chem	0.00e+00	
12	424	25.1	1495	25	HU5CCCKR1A	Human C-C chemokine re	0.00e+00	
13	424	25.1	1609	21	EL3385	cDNA encoding human MI	0.00e+00	


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REFERENCE 2 (bases 1 to 1717)
AUTHORS Daugherty,B.L.
TITLE Direct Submission
JOURNAL Submitted (13-MAR-1996) Bruce L. Daugherty, Inflammation Research,
Merck Research Laboratories, R80W-107, P.O. Box 2000, Rahway, NJ
07065, USA

FEATURES             Location/Qualifiers
     source            1..1717
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                        /db_xref="taxon:9606"
     gene              205..1272
                        /gene="CMKBR3"
     CDS                205..1272
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AVLAALPEFIFYEEELFEETLCSALXPEDTVYWRHFTLRMTIFCLVPLLYMAIC
YTGIKLLRCPKSKYKAIKIRLIFVIMAVFFIWTYPYVAILLSYLFGNDCERS
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BASE COUNT  434 a  428 c  351 g   504 t
ORIGIN
Query Match      97.0%; Score 1637; DB 25; Length 1717;
Best Local Similarity 99.3%; Pred. No. 0.00e+00;
Matches 1683; Conservative 0; Mismatches 5; Indels 7; Gaps 7;

Db      24  AATCCTCTCTGGCACCCTCTGATAGCCTTTTGAATTCATGTTAAAGAACCTCCCTAGC 83
Qy      1  AATCCTTTCTGGCACCCTCTGATAT -CCTTTTGAATTCATGTTAAAGAACCTCCCTAGC 59

Db      84  TGCTATCATGTCGATCTTTGTGAGTACATGATTAATCAATCACTGGTGTGTTTACGA 143
Qy      60  TGCTATCATGTCGATCTTTGTGAGTACATGATTAATCAATCACTGGTGTGTTTACGA 119

Db      144  AGGATGATTATGCTTCATTTGGGATGTGATTTTCTTCTATCACAGGAGGAAGTGA 203
Qy      120  AGGATGATTATGCTTCATTTGGGATGTGATTTTCTTCTATCACAGGAGGAAGTGA 179

Db      204  AATGCAACCTCACTAGATACAGTGTGAGACCTTTGGTACCACATCCTACTATGATGACGT 263
Qy      180  AATGCAACCTCACTAGATACAGTGTGAGACCTTTGGTACCACATCCTACTATGATGACGT 239

Db      264  GGGCTGCTCTGTGAAGAGCTGATACAGACGACTGATGGCCAGTTTGTGCCCCCGCT 323
Qy      240  GGGCTGCTCTGTGAAGAGCTGATACAGACGACTGATGGCCAGTTTGTGCCCCCGCT 299

Db      324  GTACTCCCTGGTGTTCACGTGGGCTCTTGGCAATGTGGTGGTGGTGGTGGTGGTGGTGGT 383
Qy      300  GTACTCCCTGGTGTTCACGTGGGCTCTTGGCAATGTGGTGGTGGTGGTGGTGGTGGTGGT 359

Db      384  AAAATACAGAGGCTCCGAATATGACCAACATCTACCTGCCTCAACCTGGCCATTTCCGA 443
Qy      360  AAAATACAGAGGCTCCGAATATGACCAACATCTACCTGCCTCAACCTGGCCATTTCCGA 419

Db      444  CTTGCTCTCTGCTGACCTCCATTCCTGATGATGATGATGATGATGATGATGATGATGATG 503
Qy      420  CTTGCTCTCTGCTGACCTCCATTCCTGATGATGATGATGATGATGATGATGATGATGATG 479

Db      504  TTTTGGCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 563
Qy      480  TTTTGGCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 539

Db      564  GATCTTTTTCATAATCCTGCTGACATGACAGGTACCTGGCCATGTCCTGCTGCTGCTG 623
Qy      540  GATCTTTTTCATAATCCTGCTGACATGACAGGTACCTGGCCATGTCCTGCTGCTGCTG 599

Db      624  TGCCCTTCGAGCCCGGACGTGTCACCTTTTGGTGTGTCATCACAGGATGTCACCTGGGGCCT 683
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KEYWORDS

SOURCE

ORGANISM

human.
Homo sapiens
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominoidea; Homo.
REFERENCE
1 (bases 1 to 1068)
Xiao, L., Welss, S., Qari, S., Rudolph, D., Hodge, T. and Lal, R.
Partial resistance to infection by syncytium-inducing primary HIV-1
in exposed uninfected individuals homozygous for CCR5 32bp deletion
Unpublished
REFERENCE
2 (bases 1 to 1068)
Qari, S.
Direct Submission
AUTHORS
TITLE
JOURNAL
Submitted (24-SEP-1997) Retrovirus Diseases Branch, Centers for
Disease Control and Prevention, 1600 Clifton Road, Atlanta, GA
30333, USA

FEATURES

source

Location/Qualifiers

1..1068

/organism="Homo sapiens"

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AVLAALPEIFVETELFEETLSALYEDPTVYVSRHFLRTIFCLVPLVLAIC
YTGIIKTLRPSKKYKALRILFVIMAVFFIFWTPYNVAILLSVSQSLFNGDCERS
KHLDVLMYLVETIAYSHCCMNPIYAFVGRFRKRLRHFHRLHMLHGRYIPFLPSE
KLRTSSVSPSAEPLSIVF"

BASE COUNT 231 a 289 c 243 g 305 t

ORIGIN

Query Match

Best Local Similarity 63.0%; Score 1064; DB 26; Length 1068;

Matches 1066; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 ATGACACCTCCTAGATACAGTTGAGACCTTTGGTACCACATCCTACTATGATGAGCTG 60
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181 ATGACACCTCCTAGATACAGTTGAGACCTTTGGTACCACATCCTACTATGATGAGCTG 240
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Db 61 GGCTGCTCTGTGAAAAGCTGATACACAGACCTGATGCCAGTTTGTGCCCGCCGCTG 120
|||||
Qy 241 GGCTGCTCTGTGAAAAGCTGATACACAGACCTGATGCCAGTTTGTGCCCGCCGCTG 300
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Db 121 TACTCCCTGGTGTCTACTGTGGGCTCTTGGGCAATGTGGTGGTGGTGGTGGTGGTGGT 180
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Qy 301 TACTCCCTGGTGTCTACTGTGGGCTCTTGGGCAATGTGGTGGTGGTGGTGGTGGTGGT 360
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Db 181 AATACAGAGGCTCCCAATATGACCAACATCTACCTGCTCAACCTGCCATTCGGAC 240
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Qy 361 AATACAGAGGCTCCCAATATGACCAACATCTACCTGCTCAACCTGCCATTCGGAC 420
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Db 241 CTGCTCTCTCTGTCACCTTCCATTTCTGATCCACTATGTGAGGGGCACTAATCGGTT 300
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Qy 421 CTGCTCTCTCTGTCACCTTCCATTTCTGATCCACTATGTGAGGGGCACTAATCGGTT 480
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Db 301 TTGGCCATGGCATGTGTAAGCTCCTCTCAGGTTTTTATCACAGAGCTTGTACAGCGAG 360
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Qy 481 TTGGCCATGGCATGTGTAAGCTCCTCTCAGGTTTTTATCACAGAGCTTGTACAGCGAG 540
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Db 361 ATCTTTTTCATATCTCTGTGACAAATCGACAGGTACCTGGCATTGTCCATGTGTGTTT 420
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Qy 541 ATCTTTTTCATATCTCTGTGACAAATCGACAGGTACCTGGCATTGTCCATGTGTGTTT 600
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Db 421 GCCCTTCGAGCCGAGCTGTCACTTTTGGTGTATCATCAGGATCGTCACTGGGCGCTG 480
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Qy	241	GGCCTGCTCTGTGAAAAAGCTGATACGAGGACCTGATGGCCCAAGTTGTGCCCCCGCTG	300
Db	121	TATTCCCTGGTGTTCATGTGTGGGCCCTCTTTGGGCAACGTGGTGGTGTGATGATCCTCAT	180
Qy	301	TACTCCTGGTGTTCATGTGTGGGCCCTCTTTGGGCAATGTGGTGGTGTGATGATCCTCAT	360
Db	181	AAATACAGAGGCTCCGAATTTATGACCAACATCTACTTGCCTCAACCTGGCCATTTCCGAC	240
Qy	361	AAATACAGAGGCTCCGAATTTATGACCAACATCTACTTGCCTCAACCTGGCCATTTCCGAC	420
Db	241	CTGCTCTTCCTCTTCAACCTTCGCTTCTGGATCCACTATGTCAAGGAGCGTAACCTGGGCT	300
Qy	421	CTGCTCTTCCTCTGACCCCTCCATTTCTGGATCCACTATGTCAAGGAGCGTAACCTGGGCT	480
Db	301	TTGAGCATGGCAATGTGAAGTCTCTCGGGGTTTTATCACACAGGCTTGTACAGCGAG	360
Qy	481	TTTGGCCATGGCAATGTGAAGTCTCTCGGGGTTTTATCACACAGGCTTGTACAGCGAG	540
Db	361	ATCTTTTTTCAATACTCTCTGACGATTGACAGTACCTTGGCCATTTGTCCATGCTGTGTT	420
Qy	541	ATCTTTTTTCAATACTCTCTGACATCGACAGTACCTTGGCCATTTGTCCATGCTGTGTT	600
Db	421	GCCTTCGAGCCAGGACTGTCACTTTTGGTGCATCTAGCATGTCACCTGGGGCCTG	480
Qy	601	GCCTTCGAGCCGAGCTGTCACTTTTGGTGCATCACGACGCTGCACCTGGGGCCTG	660
Db	481	GCAGTCTACGAGCTCTCTGAAATTTATTTCTATGGAGCTGAAGTGTGTTTCCAGAG	540
Qy	661	GCAGTCTACGAGCTCTCTGAAATTTATTTCTATGAGACTGAAGTGTGTTTGAAGAG	720
Db	541	ACTCTTTGCAGTGTCTATTTACCCGCGAGGATACAGATATATAGCTGGAGGCAATTTCCACACT	600
Qy	721	ACTCTTTGCAGTGTCTTTACCCAGAGGATACAGATATATAGCTGGAGGCAATTTCCACACT	780
Db	601	CTGAGATGACGATCTGTGTCTGCTCTCCCTCTGCTGTGTTATGGCCATCTGCTACACA	660
Qy	781	CTGAGATGACGATCTGTGTCTGCTCTCCCTCTGCTGTGTTATGGCCATCTGCTACACA	840
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Qy	841	GGATCATAAAAAGCTGTGAGTGGCCCGACGATAAAAAAGTACAAAGGCCATCCGGCTC	900
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Qy	901	ATTTTGTCTAATGAGCTGTGTTTTTCATTTTCTGGACACCTTACAATGTGGCTATCCTT	960
Db	781	ATCTCTACCTATCAATCCGCTTATTTGACATTTGACTGTGAACGGAGCAAGCATCTGGAC	840
Qy	961	CTCTCTTCTCTATCAATCCATCTATTTTGAATGACTGTGAGCGAGCAAGCATCTGGAC	1020
Db	841	CTGTTCTGCTGGCGAGGAGTGTACGCTTACTCCCACTGCTGCGTGAACCCAGTATC	900
Qy	1021	CTGGTCATGCTGCTGACAGAGTGTACGCTTACTCCCACTGCTGCATGAACCCGCTATC	1080
Db	901	TATGCCCTTTGTTGGAGAGAGTTCCGGAAGTACCTGCGCCACTTCTCCACAGGACAGTG	960
Qy	1081	TAGGCCCTTTGTTGGAGAGAGTTCCGGAAGTACCTGCGCCACTTCTCCACAGGACAGTG	1140
Db	961	CTCATGCACTGGGCAAAATACATCCCATTTCTCTAGTGAGAAGCTGGAAGAACCAGC	1020
Qy	1141	CTCATGCACTGGGCAAGATACATCCCATTTCTCTAGTGAGAAGCTGGAAGAACCAGC	1200
Db	1021	TCGTCTCTCCGTCACAGAGAGCGGAACCTCTATATGTGTTTTAG	1068
Qy	1201	TCGTCTCTCCATCCACAGAGCGGAACCTCTATATGTGTTTTAG	1248

RESULT	7	AF017283	1068 bp	DNA	PRI	18-SEP-1997
LOCUS						
DEFINITION		Macaca mulatta chemokine receptor (CCR3) gene, complete cds.				
ACCESSION		AF017283				
NID		G2407218				

KEYWORDS
SOURCE
ORGANISM
rhesus monkey.
Macaca mulatta
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.
1 (bases 1 to 1068)
Hauer,D.A., Margulies,B.J. and Clements,J.E.
Direct Submission
Submitted (05-AUG-1997) Division of Comparative Medicine, Johns
Hopkins University School of Medicine, 720 Rutland Ave., Traylor
G-60, Baltimore, MD 21205, USA

FEATURES
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Location/Qualifiers
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VTGIKLTLRCPSKKYKARLLFVIMAVEFIEFTPYNVAIILTYSOVLFLGDCCRS
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BASE COUNT 229 a 289 c 245 g 305 t
ORIGIN

Query Match 56.2%; Score 948; DB 26; Length 1068;
Best Local Similarity 94.4%; Pred. No. 0.00e+00;
Matches 1008; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

Dbb 1 ATGCAACCTCACATAGATACGGTGTCGACACTTTGGTCCACATCGTAGCATGATGCATG 60
Qyb 181 ATGCAACCTCACATAGATACAGTTGAGACCTTTGGTACCACATCCTACTATGATGACGTG 240
Dbc 61 GGTCGTCTCTGTA AAAAGCCGATGTCGGAGCACTGATPAGCCCAGTTGGTGCCCCCCGTG 120
Qyd 241 GGCCCTGCTCTGTA AAAAGCTGATACACAGACACTGATGGCCCACTTTGTCGCCCCGCTG 300
Dbe 121 TATTCCTCGGTGTTTCATGGTGGGCTCTTGGCAACGCTGGTGGTGATGATCCTCATATA 180
Qyf 301 TACTCCCTGGTGTTCACGTGGGCTCTTGGCAATGTTGGTGGTATGATCCTCATATA 360
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Qyi 421 CTGCTCTCTCTCGTCACTCTCCACTTCCTGGATCCACTATGTTCAGGAGCGCATAACTGGGTT 480
Dbi 301 TTCACCATGGCATGTGTAAAGTCTCTCGGGGTTTTATACACAGGCTTTGTACAGCGAG 360
Qyj 481 TTGGCCATGGCATGTGTAAAGTCTCTCGAGGGTTTTATACACAGGCTTTGTACAGCGAG 540
Dbj 361 ATCTTTTTTCATAATCTCTCCAGCATTCACAGGTACCTGGCCATGTCCATGCTGTGTGTTT 420
Qyk 541 ATCTTTTTTCATAATCTCTGCTGACATTCAGAGGTACCTGGCCATGTCCATGCTGTGTTT 600
Dbl 421 GCCCTTCGAGCCAGGACTGTCACTTTTGGTGTCACTACCTAGCATCGTCACCTGGGGCCTG 480
Qyl 601 GCCCTTCGAGCCGAGCTGTCACTTTTGGTGTCACTACCGAGCATCGTCACCTGGGGCCTG 660
Dbm 481 CGAGTGCTAGCAGCTCTCTCGAATTAATTTTCATGGGACTGAAAAGTGTGTTTCCAAAA 540
Qym 661 GCAGTGTCTAGCAGCTCTCCCTGAATTTATCTCTATGAGCTGAAGAGTGTGTTTGAAGAG 720

Db 541 ACTCTTTGACGTCTATTCCACAGATACATATATAGCTGGAGCATTTCCACACT 600
Qy 721 ACTCTTTGACGTCTATTCCACAGATACATATATAGCTGGAGCATTTCCACACT 780
Db 601 CTGAAATGACATCTTGCTCGCTCCCTCTGCTCGTATGAGGCATCTGTACACA 660
Qy 781 CTGAGATGACATCTTGCTCGCTCCCTCTGCTCGTATGAGGCATCTGTACACA 840
Db 661 GGAATCATCAAAACGCTGCTGAGTGCCCGCAGTAAAAAAGTACAAAGGCATCCGGCTC 720
Qy 841 GGAATCATCAAAACGCTGCTGAGTGCCCGCAGTAAAAAAGTACAAAGGCATCCGGCTC 900
Db 721 ATTTTGTGCATCATGCTGCTGCTTTTTCATTTCTGGACACCTACATGCTGGCTATCCTT 780
Qy 901 ATTTTGTGCATCATGCTGCTGCTTTTTCATTTCTGGACACCTACATGCTGGCTATCCTT 960
Db 781 ATCTCTACCTATCAATCCGCTTATTGGAGTCTGACCTGAGTGAACGAGCAAGCATCTGGAC 840
Qy 961 CTCCTCTCATCAATCCATCTTATTGGAATGACCTGTGAGCGGAGGAGCATCTGGAC 1020
Db 841 CTGTTCTGCTGGCGAGGAGTGATCGCTTACCTCCACTGCTCGTGTAACCCAGTATC 900
Qy 1021 CTGCTCATGCTGCTGACAGAGTGATCGCTTACCTCCACTGCTGCATGAACCCGCTGATC 1080
Db 901 TACGCTTTGCTGGAGAGGTTCCGGAAGTACCTGCGCCACTTCTTCCACAGCAGCTG 960
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Qy 1141 CTCATGACCTGGGCAATACATCCCATCTCTCTAGTGAGAGCTGGAAGAACACGAC 1200
Db 1021 TCTGCTCTCGCTCCACAGAGAGCCGGAACCTCTCTATGCTGTTTGTAG 1068
Qy 1201 TCTGCTCTCCATCCACAGAGAGCCGGAACCTCTCTATGCTGTTTGTAG 1248

RESULT 8
LOCUS MMU28406 1440 bp DNA ROD 27-FEB-1996
DEFINITION Mus musculus macrophage inflammatory protein-1 alpha receptor-like
2 gene, complete cds.
ACCESSION U28406
NID g1203800
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Mus.
1 (bases 1 to 1440)
Gao, J. L. and Murphy, P. M.
Cloning and differential tissue-specific expression of three mouse
beta chemokine receptor-like genes, including the gene for a
functional macrophage inflammatory protein-1 alpha receptor
J. Biol. Chem. 270 (29), 17494-17501 (1995)
95340546
MEDLINE 2 (bases 1 to 1440)
REFERENCE Gao, J. L.
AUTHORS Direct Submission
TITLE Submitted (05-JUN-1995), Ji-Liang Gao, Lab of Host Defenses, NIAID,
National Institutes of Health, Building 10, Room 11N13, Bethesda,
MD 20892, USA
COMMENT On Feb 27, 1996 this sequence version replaced gi:1199860.
FEATURES
Location/Qualifiers
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/clone_lib="lambda FIX 129/SvJ mouse genomic DNA library"
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227..1350
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receptor-like 2 gene"

CDS

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TWGLAGLAALPEFIFHESQDSFGEPCSPRYGEEDSKRHFHALRMIFGALPLLV
MYICSGIILKTLRCPNKKKRAIRLIFVMIVVFIFWTPYNLVLSFAHSTFLETS
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BASE COUNT 365 a 325 c 295 g 455 t
ORIGIN
Query Match 35.5%; Score 600; DB 28; Length 1440;
Best Local Similarity 75.9%; Pred. No. 0.00e+00;
Matches 886; Conservative 0; Mismatches 281; Indels 1; Gaps 1;
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Qy 202 GTTGAGACCTTTGGTACCATCTACTATGATGAGCTGGGCTGTCTGTGAAAAGCT 261
Db 320 AGAATCAAGAGCTGGGTCTATGCTCCTCCCTCACTGTACTCCTCGTGTTCATCATC 379
Qy 262 GATACAGAGCATGATGGCCAGTTGTGCCCCCTGTACTCCTCGTGTTCATCTGTG 321
Db 380 GGCTCTCTGGCAACATGATGGTGTGTGATCTCATAAAGTACAGGAGCTACAAAT 439
Qy 322 GGCTCTTGGCAATGTTGGTGTGTGATGATCTCATAAATACAGGAGCTCCGAAT 381
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Qy 382 ATGACCAACATCTACCTGTCAACCTGGCCATTTGGGACCTGTCTTCTTCTTCACT 441
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Qy 442 CCATTCTGATTCACATATGTTCAAGGGGCGATACCTGGGTTTGGCCACTGTGTAAG 501
Db 560 ATGCTGTCTGGGTTTATTTACCTGGCTGTGACAGGAGATCTTTTTCATCATCTGCTG 619
Qy 502 CTCTCTCAGGTTTATACACAGAGCTGTGACAGGAGATCTTTTTCATCATCTGCTG 561
Db 620 ACAATTGACAGATACCTGGCTATCGTCCATGCTGTTTGGCCCTTCGAGCCGCACTGTG 679
Qy 562 ACAATGACAGGATACCTGGCCATGTCATGCTGTCTTGTGCCCCTTCGAGCCGCACTGTG 621
Db 680 ACTTTGCTACTATCACAGTATCATCTGCGGCTTTCGAGGAGCTGGCAGCATTCGCT 739
Qy 622 ACTTTGCTACTATCACAGTATCATCTGCGGCTTTCGAGGAGCTGGCAGCATTCGCT 681
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Qy 802 CTGCTTCT 861
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Db 980 TTTTATTTTGTGGACCCCGTACAACTGGTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 1039
Qy 922 TTTTATTTTGTGGACCCCGTACAACTGGTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 981
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QY	802	CTCGTTCTCCCTCGCTGCTATGGCCATCTGCTACACAGGAATCATCAAAACGCTGCTG	861
Db	694	AGATGCCCAATAAAAAACAACAGCCATCCAGCTTATTTTGTGTCATGATAGTC	753
QY	862	AGTGCCCCAGTAAAAAAGTACAGGCCATCGGCTCATTTTGTTCATCATGGCGTG	921
Db	754	TTTTTTATTTTGGACTCCATCAACACTGGTCTTCTTCTGCTGCTTTCCACAGACACA	813
QY	922	TTTTTCATTTTGGACACCTACAATGTGCTATCCTTCTCTCTCATCAATCCATC	981
Db	814	TTTTTGGAGACAGCTGCTGACGAGAGCATACACCTGACCTGGCCATGCAAGTGACTGAG	873
QY	982	TTATTTGGAATGACTGTGAGCGGACGAAGCATCTGACCTGGTCTGCTGCTGACAGAG	1041
Db	874	GTGATTACCCACACCCACTGCTGTATCAATCAATCAATATATCTATGCTTTGTTGGTGAGGG	933
QY	1042	GTGATGCCCTACTCCCACTGCTGATCAACCGGTGATCTACGCTTGTGTGGAGAGGG	1101
Db	934	TTCCGGAACACCTTCGGCTCTTTTCCACAGAAATATGGCAATCTACCTGAGAAAAATAT	993
QY	1102	TTCCGGAAGTACCTGCGCCACTTCTCCACAGGCACCTGCTCATGCACCTGGGCGAGATAC	1161
Db	994	ATTTCATTCCTCTCGGCGAGAACTGGAAGAACAAGCTCTGCTCTCCCATCAACTGAGG	1053
QY	1162	ATCCCATTCCTCTCTAGTAGAAGCTGGAAGAACCAGCTCTGCTCTCCATCCACAGCA	1221
Db	1054	GAGCAAGAAATCTCTGTTGGTCTTTTAG	1080
QY	1222	GAGCGGAACCTCTCTATGTGTTTTAG	1248
RESULT	12		
LOCUS	HMCCCKRIA	1495 bp	mRNA
DEFINITION	Human C-C chemokine receptor type 1 (C-C CKR-1)	31-DEC-1994	
ACCESSION	L09230		
NID	g179984		
KEYWORDS	C-C chemokine receptor type 1.		
SOURCE	Homo sapiens		
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 1495)		
AUTHORS	Neote, K., DiGregorio, D., Mak, J. Y., Horuk, R. and Schall, T. J.		
TITLE	Molecular cloning, functional expression, and signaling characteristics of a C-C chemokine receptor		
JOURNAL	Cell 72 (3), 415-425 (1993)		
MEDLINE	93161416		
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Matches	695;	Mismatches 271;	Indels 0;
Conservative	0;	Gaps 0;	

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RESULT 13 E13385 1609 bp DNA PAT 27-APR-1998
LOCUS
DEFINITION cDNA encoding human MIP-1 alpha /RANTES receptor.

ACCESSION E13385
NID G3252190
KEYWORDS JP 1997176048-A/1.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1609)
Honda, S. and Fujisawa, T.
PRODUCTION OF HUMAN MIP-1ALPHA/PANTES RECEPTOR PROTEIN AND USE
Patent: JP 1997176048-A 1 08-JUL-1997;
TAKEDA CHEM IND LTD
COMMENT OS Homo sapiens (human)
PN JP 1997176048-A/1
PD 08-JUL-1997
PF 28-DEC-1995 JP 1995342130
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Best local Similarity 71.9%; Pred. No. 0.00e+00;
Matches 695; Conservative 0; Mismatches 271; Indels 0; Gaps 0;
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SOURCE	Unknown.		
ORGANISM	Unknown.		
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AUTHORS	Murphy, P. M.		
TITLE	Cloning and expression of the human macrophage inflammatory protein-1.alpha..		
JOURNAL	Patent: US 5652133-A. 1 29-JUL-1997;		
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9292416
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 macrophage inflammatory protein-1-alpha.
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 cDNA to mRNA.
 ORGANISM Homo sapiens
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 REFERENCE 1 (bases 1 to 2156)
 AUTHORS Gao, J.-L., Tiffany, H.L., Kuhns, D., McDermott, D., Li, X., Francke, U.
 and Murphy, P.M.
 TITLE Structure and functional expression of the human macrophage
 inflammatory 1 alpha (MIP-1alpha)/RANTES receptor
 J. Exp. Med. 177, 1421-1427 (1993)
 MEDLINE 93240122
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 BASE COUNT 538 a 547 c 504 g 567 t
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 Query Match 25.1%; Score 424; DB 25; Length 2156;
 Best Local Similarity 71.9%; Pred. No. 0.00e+00;
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 Db 161 GGCCCAACTGCTGCCCTCTGTACTCTGTGATTTGTCTATGGCTGGTGGAAACAT 220
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 BASE COUNT
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 Qy 1239 TGTGTT 1244

 Search completed: Tue Dec 8 22:05:07 1998
 Job time : 4555 secs.

WQISREAH (TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
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ch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Dec 8 13:14:19 1998; MasPar time 11.57 Seconds
Tabular output not generated. 496.409 Million cell updates/sec

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Perfect Score: 2765
Sequence: 1 MTTSLDIVEFGTTSYDDV.....LERTSSVSPSTAEPELSIVF 355

Scoring table: PAM 150
Gap 11

Searched: 131922 seqs, 16180660 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

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8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
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19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29

Statistics: Mean 34.824; Variance 168.421; scale 0.207

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2748	99.4	355	28 W31850	Human eosinophil eota	2.62e-228
4	2748	99.4	355	24 W27124	Human chemokine recep	2.62e-228
5	2748	99.4	355	19 W03377	CC-chemokine receptor	2.62e-228
6	2710	98.0	356	26 W25943	Human CCR3 chemokine	6.22e-225
7	2658	96.1	355	19 W03378	CC-chemokine receptor	2.58e-220
8	1828	66.1	355	11 R52749	C-C chemokine recepto	8.66e-147
9	1828	66.1	355	25 W26588	Human MIP-1 alpha/RAN	8.66e-147
10	1828	66.1	355	24 W25751	Human MIP-1alpha/RANT	8.66e-147
11	1720	62.2	355	24 W29179	Rat CC chemokine rece	2.96e-137
12	1509	54.6	352	24 W27125	Macaque chemokine rec	1.17e-118
13	1496	54.1	352	24 W27123	Human chemokine recep	1.63e-117
14	1496	54.1	352	27 W27407	Human CCR5	1.63e-117
15	1496	54.1	352	29 W23835	Human CC chemokine re	1.63e-117
16	1497	54.1	371	29 W23834	Human CC chemokine re	1.33e-117
17	1483	53.6	352	20 W07602	Human G-protein chemo	2.27e-116
18	1438	52.0	360	14 R79166	Human monocyte chemoa	2.06e-112

19	1438	52.0	360	26 W35833	Human monocyte chemoa	2.06e-112
20	1390	50.3	332	28 W26766	Human chemokine recep	3.41e-108
21	1352	48.9	374	14 R79165	Human monocyte chemoa	7.43e-105
22	1251	45.2	360	19 R99274	Chemokine receptor K5	5.40e-96
23	1079	39.0	355	20 W07618	Human G-protein recep	6.04e-81
24	1006	36.4	355	11 R53748	Seven transmembrane r	1.41e-74
25	934	33.8	356	29 W48087	Human macrophage/dend	2.60e-68
26	921	33.3	344	28 W26767	Human chemokine recep	3.51e-67
27	816	29.5	358	11 R53745	Partial sequence of s	4.46e-58
28	816	29.5	410	11 R53743	Putative seven trans	4.46e-58
29	813	29.4	378	11 R53744	Putative seven trans	8.11e-58
30	804	29.1	184	27 W27406	Inactive human CCR5	4.87e-57
31	804	29.1	215	27 W27408	Inactive human CCR5	4.87e-57
32	793	28.7	365	29 W48086	Human dendritic cell	4.35e-56
33	787	28.5	378	10 R54079	Epstein Barr virus in	1.43e-55
34	756	27.3	359	11 R53747	Seven transmembrane r	6.81e-53
35	738	26.7	355	7 R33420	Human IL-8 receptor f	2.43e-51
36	738	26.7	360	6 R28273	Sequence in a low aff	2.43e-51
37	738	26.7	1064	14 R70124	IL8-R type 2-GBP 130	2.43e-51
38	738	26.7	360	15 R80758	Recombinant high affi	3.90e-50
39	724	26.2	350	15 R80951	Interleukin-8 recepto	3.90e-50
40	724	26.2	350	12 R68811	Interleukin-8 recepto	3.90e-50
41	724	26.2	350	15 R80756	Human G-protein chemo	3.90e-50
42	724	26.2	415	23 W19780	IL8-R type 1-GBP 130	3.90e-50
43	724	26.2	1060	14 R70123	Recombinant high affi	8.61e-50
44	720	26.0	360	15 R80953	Interleukin-8 recepto	1.56e-49
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ALIGNMENTS

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AC W03376;
DT 15-NOV-1996 (first entry)
DE CC-chemokine receptor 3;
KW CC-chemokine receptor 3; CKP-3; Eos-L2; inhibitor; antisense;
KW antiinflammatory; eosinophil.
OS Homo sapiens.
FH Key Location/Qualifiers
FT region 130..138
FT /note= "amino acids 130-138 comprise a motif
FT conserved among C-X-C and C-C chemokine
FT receptors"

W09622371-A2.
PD 25-JUL-1996.
PF 19-JAN-1996; U00608.
PR 19-JAN-1995; US-375199.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
PA (CHIL) CHILDRENS MEDICAL CENT.
PA (LEUK) LEUKOSITE INC.
PI Gerard CJ, Gerard NP, Mackay CR, Ponath PD, Post TW;
PI Qin S;
PI WPI; 96-354528/35.
DR N-PSDB; T31334.
DR Mammalian chemokine receptor-3 and related nucleic acids - useful to
PT identify receptor inhibitors to treat inflammatory disease, e.g.
PT autoimmune disorders, certain cancers, etc.
PS Claim 10; Page 110-111; 153pp; English.
CC A novel human receptor (W03376), designated Eos L2 or C-C chemokine
CC receptor 3 (CCR-3), is involved in leukocyte migration associated
CC with inflammation. Its sequence was deduced from a genomic DNA
CC clone (T31334). A slightly different amino acid sequence (W03377)
CC was deduced from a cDNA clone (T31335), and a consensus sequence
CC is given in W03378. Recombinant CCR-3 can be produced in host
CC cells, and is useful for screening for CCR-3 ligands, promoters
CC and inhibitors. The inhibitors can be used to treat inflammatory
CC disease.
SQ Sequence 355 AA;
Query Match 99.5%; Score 2751; DB 19; Length 355;
Best Local Similarity 99.7%; Pred. No. 1.42e-228;
Matches 354; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 mtsldtvetfqttsydvglcekadtralmagfvpplyslvftvgllgnvmmili 60
 Qy 1 MTSLDTVEFTGTSYDDVGLCEKADTRALMAQFVPPPLYSLVFTFGLLGNVMMILI 60
 Db 61 kyririntniylnlainsdlflvtlpfwhvgrhwnvghgmckllsgfyhtglyse 120
 Qy 61 KYRRLRINTNIYLLNLAISDLFLVTFPWHVYGRHWNVFGHGMCKLLSGFYHTGLYSE 120
 Db 121 iffiilltidrylaivhavfalrartvtfvgitsvwtglavlaalpefifeteelfee 180
 Qy 121 IFFIILLTIDRYLAIVHAVFALRARTVTFVGITSVWTGLAVLAALPEFIFETEELFEE 180
 Db 181 tlcsalypedtyvsrwhfhlrtmifclvlpplvmaicytgiiktlrcpskkykairl 240
 Qy 181 TLCSALYPEDTYVSRWHFHLRTMIFCLVLPPLVMAICYTGIKTLRCPSSKKYKAIRL 240
 Db 241 ifvimaavffitwpyvnaillssyqsilfndcckhldvmlvteviayshccmpvi 300
 Qy 241 IFVIMAVFFITWPPYNVAILLSSYQSILFNDCKHLDVMLVTEVIAYSHCCMPVI 300
 Db 301 yafvgerfkrlyrhffrhlmlhlgryipflpseklerstssvstapelsivf 355
 Qy 301 YAFVGERFKRLYRHFHRLMLHLGRIYIPFLPSEKLERSTSSVSTAPELSIVF 355

RESULT 2
 ID W10100 standard; Protein: 355 AA.
 AC W10100;
 DT 30-SEP-1997 (first entry)
 DE Human C-C chemokine receptor 3.
 KW Human; eotaxin; eosinophil; chemoattractant; stimulation;
 KW accumulation; attraction; chemotaxis; diagnosis; prevention;
 KW treatment; disease; inflammation; allergy; asthma; rhinitis;
 KW hypersensitivity; lung; pneumonia; Loeffler's; syndrome;
 KW interstitial; ILD; idiopathic pulmonary fibrosis;
 KW rheumatoid arthritis; systemic; lupus erythematosus; SLE;
 KW ankylosing spondylitis; sclerosis; Sjogren's; polymyositis;
 KW dermatomyositis; bowel; anaphylaxis; drug; penicillin;
 KW cephalosporin; insect sting; Crohn's; ulcerative colitis;
 KW spondyloarthropathy; scleroderma; psoriasis; dermatosis;
 KW dermatitis; eczema; atopic; urticaria; necrotizing; cutaneous;
 KW vasculitis; myositis; fascitis; multiple sclerosis;
 KW myasthenia gravis; juvenile onset diabetes; glomerulonephritis;
 KW autoimmune; thyroiditis; Bechet's; graft; rejection;
 KW transplantation; allograft; graft versus host; cancer;
 KW leukocyte infiltration; reperfusion injury; atherosclerosis;
 KW haematologic malignancy; septic; endotoxic; shock;
 KW polymyositis; dermatomyositis; immunosuppression; immunodeficiency;
 KW AIDS; radiation therapy; chemotherapy; autoimmune; corticosteroid;
 KW C-C chemokine receptor 3; CRK3.
 Homo sapiens.
 PW W09700960-A1.
 PD 09-JAN-1997.
 PE 21-JUN-1996; U10723.
 PR 23-JUN-1995; US-494093.
 PA (LEUK-) LEUKOSITE INC.
 PI Mackay C, Newman W, Ponath PD, Qin S, Ringler DJ;
 DR WPI; 97-087387/08.
 DR N-PSDB; T58783.
 PT New isolated human eotaxin gene - used to develop prods. for the
 PT diagnosis and treatment of e.g. inflammation, allergies, auto-immune
 PT disease, infections and tumours
 PS Example 7; Pages 98-99; 130pp; English.
 CC The present sequence is human C-C chemokine receptor 3 (CRK3),
 CC to which human eotaxin (hE), an eosinophil specific chemoattractant
 CC capable of stimulating eosinophil accumulation and/or attracting
 CC eosinophils (including chemotaxis), binds.
 CC hE can be used to develop products for the diagnosis, prevention or
 CC treatment of hE associated diseases or conditions. The products can
 CC be used to treat inflammatory or allergic diseases and conditions,
 CC including respiratory allergic diseases (e.g. asthma, allergic
 CC rhinitis, hypersensitivity lung diseases or pneumonia).

CC eosinophilic pneumonias such as Loeffler's syndrome and chronic
 CC eosinophilic pneumonia, interstitial lung diseases (ILD) such as
 CC idiopathic pulmonary fibrosis or ILD associated with rheumatoid
 CC arthritis, systemic lupus erythematosus (SLE), ankylosing
 CC spondylitis, systemic sclerosis, Sjogren's syndrome, polymyositis
 CC or dermatomyositis), systemic anaphylaxis or hypersensitivity
 CC responses, drug allergies (e.g. to penicillin and cephalosporins),
 CC insect sting allergies, inflammatory bowel diseases (e.g. Crohn's
 CC disease and ulcerative colitis), spondylarthropathies,
 CC scleroderma, psoriasis and inflammatory dermatoses (e.g.
 CC dermatitis, eczema, atopic dermatitis, allergic contact dermatitis,
 CC urticaria and necrotizing, cutaneous and hypersensitivity
 CC vasculitis) eosinophilic myositis and fascitis, multiple
 CC sclerosis, SLE, myasthenia gravis, juvenile onset diabetes,
 CC glomerulonephritis, autoimmune thyroiditis, Bechet's disease, graft
 CC rejection (e.g. in transplantation) including allograft rejection or
 CC graft versus host disease and cancers with leukocyte infiltration
 CC of the skin or organs. The products can also be used to treat other
 CC diseases or conditions requiring the inhibition of undesirable
 CC inflammatory responses, including reperfusion injury,
 CC atherosclerosis, certain haematologic malignancies, cytokine
 CC induced toxicity (e.g. septic or endotoxic shock), polymyositis,
 CC dermatomyositis, immunosuppression (e.g. in individuals with
 CC immunodeficiency syndromes such as AIDS, undergoing radiation
 CC therapy, chemotherapy, therapy for autoimmune disease or other drug
 CC therapy, such as corticosteroid therapy, which causes
 CC immunosuppression), immunosuppression due to (e.g. congenital)
 CC deficiency (e.g. in eotaxin) or infectious diseases such as parasitic
 CC diseases.
 CC Degenerate primers based on the guinea pig eotaxin amino acid
 CC sequence were used for the reverse transcriptase polymerase chain
 CC reaction (RT-PCR) amplification of RNA isolated from inflamed,
 CC eosinophilic lung tissue obtained from Balb/c mice sensitised to
 CC ovalbumin. The amplification product was used as a probe to screen
 CC a human genomic library in vector EMBL3 SP6/T7 to obtain the hE
 CC gene.
 SQ Sequence 355 AA;
 Query Match 99.5%; Score 2751; DB 23; Length 355;
 Best Local Similarity 99.7%; Pred. No. 1.42e-228;
 Matches 354; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 1 mtsldtvetfqttsydvglcekadtralmagfvpplyslvftvgllgnvmmili 60
 Qy 1 MTSLDTVEFTGTSYDDVGLCEKADTRALMAQFVPPPLYSLVFTFGLLGNVMMILI 60
 Db 61 kyririntniylnlainsdlflvtlpfwhvgrhwnvghgmckllsgfyhtglyse 120
 Qy 61 KYRRLRINTNIYLLNLAISDLFLVTFPWHVYGRHWNVFGHGMCKLLSGFYHTGLYSE 120
 Db 121 iffiilltidrylaivhavfalrartvtfvgitsvwtglavlaalpefifeteelfee 180
 Qy 121 IFFIILLTIDRYLAIVHAVFALRARTVTFVGITSVWTGLAVLAALPEFIFETEELFEE 180
 Db 181 tlcsalypedtyvsrwhfhlrtmifclvlpplvmaicytgiiktlrcpskkykairl 240
 Qy 181 TLCSALYPEDTYVSRWHFHLRTMIFCLVLPPLVMAICYTGIKTLRCPSSKKYKAIRL 240
 Db 241 ifvimaavffitwpyvnaillssyqsilfndcckhldvmlvteviayshccmpvi 300
 Qy 241 IFVIMAVFFITWPPYNVAILLSSYQSILFNDCKHLDVMLVTEVIAYSHCCMPVI 300
 Db 301 yafvgerfkrlyrhffrhlmlhlgryipflpseklerstssvstapelsivf 355
 Qy 301 YAFVGERFKRLYRHFHRLMLHLGRIYIPFLPSEKLERSTSSVSTAPELSIVF 355

RESULT 3
 ID W31850 standard; Protein: 355 AA.
 AC W31850;
 DT 07-MAY-1998 (first entry)
 DE Human eosinophil eotaxin receptor protein CC CRK3.
 KW Eosinophil eotaxin receptor; CC CRK3; human; treatment; dermatitis;

KW atopoc condition; allergic rhinitis; conjunctivitis; bronchial asthma;
 KW beta-chemokine receptor; viral infection.
 OS Homo sapiens.
 PN W09741154-A1.
 PD 06-NOV-1997. 006568.
 PR 24-APR-1997; PF 17-JAN-1997; GB-000894.
 PR 26-APR-1996; US-016158.
 PR 26-APR-1996; US-017113.
 PA (MERL) MERCK & CO INC.
 PI Daugherty BL, Demartino JA, Siciliano SJ, Springer MS;
 DR WPI; 97-549685/50.
 DR N-PSDB; T93601.
 PT New isolated human eosinophil eotaxin receptor - used to develop
 PT products for treating and preventing atopoc conditions e.g. allergic
 PT rhinitis, dermatitis, conjunctivitis and bronchial asthma
 PT Claim 5: Page 15; 51pp; English.
 CC This is a human eosinophil eotaxin receptor. The 5099 base pair encoding
 CC cDNA sequence comprises a 1065 base pair open reading frame encoding this
 CC 355 amino acid eosinophil eotaxin receptor protein, flanked by a 5',
 CC genomic DNA sequence and a 3' terminator region. This novel eosinophil
 CC eotaxin receptor is a human beta-chemokine receptor designated CC KKR3.
 CC Agents which bind to this eosinophil eotaxin receptor can be used for
 CC the treatment and prevention of atopoc conditions such as allergic
 CC rhinitis, dermatitis, conjunctivitis and bronchial asthma. Agents which
 CC block this eosinophil eotaxin receptor can be used to prevent viral
 CC infection in healthy individuals and slow or halt viral progression
 CC in infected patients.
 SQ Sequence 355 AA;

Query Match 99.4%; Score 2748; DB 28; Length 355;
 Best Local Similarity 99.4%; Pred. No. 2.62e-228;
 Matches 353; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 mtsldtvetgtsydyddvgllcekadtralmagfvpplyslvftvgllgnvvvmili 60
 |||||
 QY 1 MTSLSLDTVETGTSYDYDDVGLLCEKADTRALMAQFVPLYSLVFTVGLGNVVVMILI 60
 |||||

Db 61 kyrllrimtniylnlaisdllflvlpfwhvgrhwnvfhgmkcllsgfyhtglyse 120
 |||||
 QY 61 KYRRLRIMTNIYLLNLAISSDLLFLVLPFWIHYVRGHNWVFGHGMCKLLSGFYHTGLYSE 120
 |||||

Db 121 iffiilltdridylaivhvfalrartvfgitsvltwglavlaalpefifeteelsee 180
 |||||
 121 IFIILLTIDRILAIVHAVFALRARTVFGITSVLTWGLAVLAALPEFIFETEELSEE 180
 |||||

QY 181 tlcsalypedvyswrhftlrmfclvlpvlmaicytgiiktllrcpskkkykairl 240
 |||||
 181 TLCSALYPEDTVYSWRHFHFLRMFICLVLPVLLVMAICYTGIKTLRCPSKKKYKAIRL 240
 |||||

Db 241 ifvmaffifwtpynvallsyqsilfgndcerskhlldvmlvteviayshccmnpvi 300
 |||||
 QY 241 IFVMAFFIFWTPYNVAILSSYQSIILFGNDCERTKHLDLVMLVTEVIAYSHCCMNPVI 300
 |||||

Db 301 yafvgerfrkylrhffhrhlmlhlgryipfipseklertssvspstaepelsivf 355
 |||||
 QY 301 YAFVGERFRKYLRFHFRHLLMLHGRYPFIPLPSEKLERTSVSSVSPSTAEPELSIVF 355
 |||||

RESULT 4
 ID W27124 standard; Protein; 355 AA.
 AC W27124;
 DT 14-DEC-1997 (first entry)
 DE Human chemokine receptor 88-2B.
 KW Chemokine receptor 88-2B; atherosclerosis; rheumatoid arthritis;
 KW tumour; asthma; viral infection; AIDS; inflammation;
 KW autoimmune disease; therapy; diagnosis; leukocyte trafficking;
 KW G protein coupled receptor; ligand; modulator; antibody; human.
 OS Homo sapiens.
 FH Key
 FT 1..36 Location/Qualifiers
 FT domain /label= Extracellular_domain
 FT domain 60..71

FT domain /label= Intracellular_domain
 FT 93..107
 FT domain /label= Extracellular_domain
 FT 131..151
 FT domain /label= Intracellular_domain
 FT 171..196
 FT domain /label= Extracellular_domain
 FT 219..240
 FT domain /label= Intracellular_domain
 FT 263..284
 FT domain /label= Extracellular_domain
 FT 306..355
 FT domain /label= Intracellular_domain
 PN W09722698-A2.
 PD 26-JUN-1997. U20759.
 PF 20-DEC-1996; U20759.
 PR 07-JUN-1996; US-661393.
 PR 20-DEC-1995; US-575967.
 PA (ICOS-) ICOS CORP.
 PI Gray PW, Raport CJ, Schweickart VL;
 DR WPI; 97-341689/31.
 DR N-PSDB; T85162.
 PT New nucleic acid encoding chemokine receptors 88-2B and 88C - used
 PT to modulate leukocyte trafficking, e.g. for treatment of
 PT inflammation, tumours, viral infections, autoimmune diseases, etc.
 PS Claim 1: Page 50-51; 65pp; English.
 CC This polypeptide sequence comprises novel human chemokine receptor
 CC 88-2B, a G protein coupled receptor that is involved in leukocyte
 CC trafficking. Its amino sequence was deduced from a cDNA clone
 CC (T85162) isolated from a macrophage library. It shows 72% identity
 CC to CCKR1. Chemokine receptor 88C (see W27123) has also been
 CC identified. 88C and 88-2B receptors and their polypeptide fragments
 CC can be produced in transformed host cells. The receptors, peptides
 CC comprising one or more of the extracellular or intracellular
 CC domains, and anti-receptor antibodies can be used to modulate
 CC receptor activities, particularly ligand and G protein binding, and
 CC are potentially useful in the treatment of
 CC atherosclerosis, rheumatoid arthritis, tumours, asthma, viral
 CC infection, AIDS, inflammatory conditions, pathological immune
 CC response, abnormal haematopoietic processes etc.
 SQ Sequence 355 AA;

Query Match 99.4%; Score 2748; DB 24; Length 355;
 Best Local Similarity 99.4%; Pred. No. 2.62e-228;
 Matches 353; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 mtsldtvetgtsydyddvgllcekadtralmagfvpplyslvftvgllgnvvvmili 60
 |||||
 QY 1 MTSLSLDTVETGTSYDYDDVGLLCEKADTRALMAQFVPLYSLVFTVGLGNVVVMILI 60
 |||||

Db 61 kyrllrimtniylnlaisdllflvlpfwhvgrhwnvfhgmkcllsgfyhtglyse 120
 |||||
 QY 61 KYRRLRIMTNIYLLNLAISSDLLFLVLPFWIHYVRGHNWVFGHGMCKLLSGFYHTGLYSE 120
 |||||

Db 121 iffiilltdridylaivhvfalrartvfgitsvltwglavlaalpefifeteelsee 180
 |||||
 QY 121 IFIILLTIDRILAIVHAVFALRARTVFGITSVLTWGLAVLAALPEFIFETEELSEE 180
 |||||

Db 181 tlcsalypedvyswrhftlrmfclvlpvlmaicytgiiktllrcpskkkykairl 240
 |||||
 QY 181 TLCSALYPEDTVYSWRHFHFLRMFICLVLPVLLVMAICYTGIKTLRCPSKKKYKAIRL 240
 |||||

Db 241 ifvmaffifwtpynvallsyqsilfgndcerskhlldvmlvteviayshccmnpvi 300
 |||||
 QY 241 IFVMAFFIFWTPYNVAILSSYQSIILFGNDCERTKHLDLVMLVTEVIAYSHCCMNPVI 300
 |||||

Db 301 yafvgerfrkylrhffhrhlmlhlgryipfipseklertssvspstaepelsivf 355
 |||||
 QY 301 YAFVGERFRKYLRFHFRHLLMLHGRYPFIPLPSEKLERTSVSSVSPSTAEPELSIVF 355
 |||||

RESULT 5
 ID W03377 standard; Protein; 355 AA.

Db 59 lvqykrlnkmtsiylnlnaisdlflfltpfwidwvfgdamckilsgfytygl 118
 Qy 59 LIKYRLRIMINILNLAISDLFLVLPFWIHVVRGHNWVFGHCKLUSGFYHTGLY 118
 Db 119 seiffiilltdrylaihvafalrartvtgvtitsiilwalaalaspnglyfskttwef 178
 Qy 119 SEIFFIILLTDRLYLAIHVAFALRARTVTGVTITSIVTWGLAVLAALPEFIFETEELF 178
 Db 179 thhtcslnhphesrwlkfgalklnlglvlpvlmlyctgtikilrrpnekkskav 238
 Qy 179 THHTCSLNHPHESRWLKFGALKLNGLVLPVLMLYCTGTIKILRRPNEKSKYKAI 238
 Db 239 rlfvimiiffllwtpyntlflsvfqlfthceqsrhldlavqvtvlaythccvnp 298
 Qy 239 RLIFVIMAVFIFWTPYNVAILSSYQISILFGNDCERTKHLDLVNLVTEVAYSHCCMNP 298
 Db 299 viyafvgerfrkylrqlfhrvavhlvkwplfslvdrlysvstspstgehelsagf 355
 Qy 299 VIYAFVGERFRKYLRFHFRHLLMHLGRYIFLPSEKLERISSVSPSTAEPELSIVF 355

RESULT 10
 ID W25751 standard; Protein; 355 AA.
 AC W25751;
 DT 20-NOV-1997 (first entry)
 DE Human MIP-1 alpha/RANTES receptor protein.
 KW Human MIP-1 alpha/RANTES receptor; osteoporosis; pCCR; digestive ulcer;
 KW macrophage inflammatory protein 1 alpha; diabetes; central disease;
 KW regulated on activation, normal T cell expressed and secreted; allergy;
 KW affinity compound; expression vector; CHO cell; viral disease;
 KW infectious disease; tumour; hyperlipidaemia; hypercholesterolaemia.
 OS Homo sapiens.
 PN J09176048-A.
 PD 08-JUL-1997.
 PE 28-DEC-1995; 342130.
 PR 28-DEC-1995; JP-342130.
 PA (TAKE) TAKEDA CHEM IND LTD.
 DR WPI; 97-399449/37.
 DT Preparation of human MIP-1-alpha/RANTES receptor protein - used in
 PT the treatment of viral diseases, tumours, allergy, diabetes
 PT osteoporosis etc.
 PS Disclosure; Page 15-16; 19pp; Japanese.
 CC This sequence represents human MIP-1 alpha/RANTES receptor (macrophage
 CC inflammatory protein 1 alpha/regulated on activation, normal T cell
 CC expressed and secreted). The human MIP-1 alpha/RANTES receptor protein
 CC may be used in a method for the screening of human MIP-1 alpha/RANTES
 CC receptor affinity compounds. The MIP-1 alpha/RANTES receptor coding
 CC sequence may be included in an expression vector, preferably pCCR, and
 CC used to transform a CHO cell for use in the same method. The receptor
 CC protein can provide a preventive and treating agent for viral diseases,
 CC infectious diseases, tumours, allergy, diabetes, central diseases,
 CC hyperlipidaemia, hypercholesterolaemia, osteoporosis, digestive ulcers,
 CC etc.
 SQ Sequence 355 AA;

Query Match 66.1%; Score 1828; DB 24; Length 355;
 Best Local Similarity 62.7%; Pred. No. 8,666-147;
 Matches 224; Conservative 68; Mismatches 61; Indels 4; Gaps 4;
 Db 1 metp-nttedydttefydgdatp-cqkvnerafagallpplyslvfvgilvgnllvvlv 58
 Qy 1 MTTSLSDTVETFGTTS-Y-YDVGGLCEKADTRALMAQVPPPLYSLVFTFGLLGNVVMVI 58
 Db 59 lvqykrlnkmtsiylnlnaisdlflfltpfwidwvfgdamckilsgfytygl 118
 Qy 59 LIKYRLRIMINILNLAISDLFLVLPFWIHVVRGHNWVFGHCKLUSGFYHTGLY 118
 Db 119 seiffiilltdrylaihvafalrartvtgvtitsiilwalaalaspnglyfskttwef 178
 Qy 119 SEIFFIILLTDRLYLAIHVAFALRARTVTGVTITSIVTWGLAVLAALPEFIFETEELF 178
 Db 179 thhtcslnhphesrwlkfgalklnlglvlpvlmlyctgtikilrrpnekkskav 238

Qy 179 BETLCSALYPEDTVYSWRHFHTLRMTIFCLVPLLVMAICYTGIIKTLRCPSSKKYKAI 238
 Db 239 rlfvimiiffllwtpyntlflsvfqlfthceqsrhldlavqvtvlaythccvnp 298
 Qy 239 RLIFVIMAVFIFWTPYNVAILSSYQISILFGNDCERTKHLDLVNLVTEVAYSHCCMNP 298
 Db 299 viyafvgerfrkylrqlfhrvavhlvkwplfslvdrlysvstspstgehelsagf 355
 Qy 299 VIYAFVGERFRKYLRFHFRHLLMHLGRYIFLPSEKLERISSVSPSTAEPELSIVF 355

RESULT 11
 ID W29179 standard; Protein; 355 AA.
 AC W29179;
 DT 19-DEC-1997 (first entry)
 DE Rat CC chemokine receptor.
 KW rat; CC chemokine receptor; screen; binding; ligand.
 OS Rattus rattus.
 PN J09227599-A.
 PD 02-SEP-1997.
 PE 22-FEB-1996; 035192.
 PR 22-FEB-1996; JP-035192.
 PA (TAKE) TAKEDA CHEM IND LTD.
 DR WPI; 97-486426/45.
 DT CC chemokine receptor protein - useful to screen for novel binding
 PT compounds
 PS Claim 1; Page 20-21; 26pp; Japanese.
 CC This sequence is a rat CC chemokine receptor. The receptor can be used
 CC to screen for novel binding compounds and for preparation of antibodies
 CC or antiserum.
 SQ Sequence 355 AA;

Query Match 62.2%; Score 1720; DB 24; Length 355;
 Best Local Similarity 57.3%; Pred. No. 2,966-137;
 Matches 204; Conservative 89; Mismatches 61; Indels 2; Gaps 2;
 Db 1 meis-niteyptttdydygdstpcqkdvrafgagllpplyslvfvgilvgnllvvlv 59
 Qy 1 MTTSLSDTVETFGTTSYD-DVGGLCEKADTRALMAQVPPPLYSLVFTFGLLGNVVMVI 59
 Db 60 mqhrslgmsltylnlfnlavsdvflfltpfwidwvfgdamckilsgfytygl 119
 Qy 60 IKYRLRIMINILNLAISDLFLVLPFWIHVVRGHNWVFGHCKLUSGFYHTGLY 119
 Db 120 eiffiilltdrylaihvafalrartvtgvtitsiilwalaalaspalckaqwef 179
 Qy 120 EIFFIILLTDRLYLAIHVAFALRARTVTGVTITSIVTWGLAVLAALPEFIFETEELF 179
 Db 180 htcsphfpdeslktwrfqalnlqlilpvlmlyctgtikilrrpnekkskav 239
 Qy 180 ETLCSALYPEDTVYSWRHFHTLRMTIFCLVPLLVMAICYTGIIKTLRCPSSKKYKAI 239
 Db 240 lifaillflwtpyntlflsvfqlfthceqsrhldlavqvtvlaythccvnp 299
 Qy 240 LIFVIMAVFIFWTPYNVAILSSYQISILFGNDCERTKHLDLVNLVTEVAYSHCCMNP 299
 Db 300 iylvvgerfrkylrqlfhrvavhlvkwplfslvdrlysvstspstgehelsagf 355
 Qy 300 IYAFVGERFRKYLRFHFRHLLMHLGRYIFLPSEKLERISSVSPSTAEPELSIVF 355

RESULT 12
 ID W27125 standard; Protein; 352 AA.
 AC W27125;
 DT 14-DEC-1997 (first entry)
 DE Macaque chemokine receptor 88C.
 KW Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis;
 KW tumour; asthma; viral infection; AIDS; inflammation;
 KW autoimmune disease; therapy; diagnosis; leukocyte trafficking;
 KW G protein coupled receptor; ligand; modulator; antibody.
 OS Macaca sp.

QY 202 RMTIFCLVPLVMAICYTGIIKTLRCPS-KKKYKAIRLIFVIMAVFFIFWTPYNVAIL 260
Db 257 lntfgef-fglncssnrlldqamqvtetlgmthccinpiiyafvgekfrnyllvffqkh 315
QY 261 LSSYQSILFG-NDCERTKHLDLVNLVTEVIAYSHCCMNPIYAFVGERFRKYLRRHFFRH 319
Db 316 iakrfckccsifqgeaperassvytrstgeqelsv 350
QY 320 LLMHLCRYIPFLPEKLERISSV-SPSTAEPELSI 353

Search completed: Tue Dec 8 13:15:18 1998
Job time : 59 secs.

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strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGAGCGCGCAATTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified p773 vector (Pharmacia). Library went through one round of normalization to a Cot - 5. Library constructed by Bento Soares and M. Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NDH19W." /db_xref="taxon:9606" /clone="298977" /clone_lib="Soares fetal lung NBHL19W" /dev_stage="19 weeks" /lab_host="DH10B (ampicillin resistant)" <1. >450

mRNA
BASE COUNT 91 a 118 c 109 g 130 t 2 others
ORIGIN

Query Match 12.1%; Score 204; DB 20; Length 450;
Best Local Similarity 80.3%; Pred. No. 0.00e+00;
Matches 297; Conservative 0; Mismatches 69; Indels 4; Gaps 4;

47 TGCCCCCTCTGCTACTCTTGGTATTGTCATTTGGCTGGTGGAAACATCTCTGGTGGTCC 106
QY 290 TCCCCCCCTGCTACTCTTGGTATTGTCATTTGGCTGGTGGAAACATCTCTGGTGGTGA 349
Db 107 TGGTCTCTGTCATACAGAGGCTTAAACATGACAGCATCTACCTCTGAACTGG 166
QY 350 TGATCTCTATAAATACAGGAGCTCCGAATATGACCAACATCTACCTGCTCACTGG 409
Db 167 CCAATTCAGCTGCTCTCTCTGTCAGCTTCCCTTCTGATGACGACGACGATGGAAG 226
QY 410 CCAATTCGAGCTGCTCTCTCTGTCAGCTTCCCTTCTGATGACGACGACGATGGAAG 469
Db 227 ATGACTGGTGTCTGTCATGCTGTCATGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 286
QY 470 ATACTGGGTGTCTGTCATGCTGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 529
Db 287 TGTACAGCGAAGATCTTTTTCATCATCTGCTGACGATGACAGTACCTGCTGCTGCTGCTGCT 346
QY 530 TGTACAGCGA-GATCTTTTTCATATCTGCTGACAAATCGACAGTACC-TGGCCATT-G 586
Db 347 TCCAGCGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 406
QY 587 TCCATGCTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 645
Db 407 ATCATTTGGG 416
QY 646 GTACCTGGG 655

RESULT 2 AA547303 542 bp mRNA EST 05-AUG-1997
LOCUS vk28h04.r1 Soares mouse mammary gland NbMMG Mus musculus cDNA clone
DEFINITION 947959 5' similar to SW:CKR2.HUMAN P41597 MONOCYTE CEMOATTRACTANT
PROTEIN 1 RECEPTOR ; mRNA sequence.

ACCESSION AA547303
NID G2308594
KEYWORDS EST.
SOURCE house mouse.

ORGANISM Mus musculus

Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
Murinae; Mus.

REFERENCE 1 (bases 1 to 542)

AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennan,G., Soares,B., Wilton,R. and
Waterston,R.

TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)

COMMENT

Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:544815

High quality sequence stop: 286.

FEATURES
source

Location/Qualifiers
1. .542
/organism="Mus musculus"
/strain="C57BL/6J"
/note="Organ: mammary gland; Vector: pT73D-Pac
(Pharmacia) with a modified polylinker; Site 1: Not I;
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5'
TGTACCAATCTGAAGTGGAGCGCGCAATTTT-3'];
T 3'];
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified p773 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M. Fatima
Bonaldo."

/db_xref="taxon:10090"
/clone="947959"
/clone_lib="Soares mouse mammary gland NbMMG"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"

<1. >542

mRNA 131 a 126 c 113 g 172 t
BASE COUNT

ORIGIN

Query Match 7.0%; Score 119; DB 8; Length 542;
Best Local Similarity 66.1%; Pred. No. 1.85e-196;
Matches 295; Conservative 0; Mismatches 146; Indels 5; Gaps 5;

6 TCACAGGCTCTATCACATTTGGTATTATTTGGTGAATCTCTTTCATTCCTCTCTGACAA 65
QY 506 TCTCAGGGTTTATCACACAGGCTTGACAGGAGATCTTTTTCATATCTCTGTCACAA 565
Db 66 TTGATAGTACTTGGCTATTCTCCATCTGTTTGTCTTTAAAGTCAGAACGTCACACT 125
QY 566 TCGACAGTACTGGCCATTTGCTGTTTGTCTTTTAAAGTCAGAACGTCACACT 625
Db 126 TTGGGTGATAACAAGTGTAGTCACTTGGGGGTGGGCTGTGTTCCTCTCTCCAGAAA 185
QY 626 TTGCTGTCATCACAGCATCTCACTTGGGCTGGAGCTGTCAGTCTCTCTGAAT 685
Db 186 TAATCTTTACAGATCTCAGAAAGAGTTTTCATATATACATGAGTCTCATTTTCAC 245
QY 686 TTATCTTCTATGAGATGAGAGTTTGTGAAGAGACTCTTTGACGTCCTTTTACCCAG 745
Db 246 ACACCT-CAGTATCATTTCTGGAAGAGTTTCCAAACATTAAGATGGTCACTCTGAGCTG 304
QY 746 AGGATACAGTAT-ATAGCTGGAGCATTTTCCACACTCTGAGATGAGCATCTCTGTCTC 804
Db 305 ATCTGCTCTTACTTGTTCATCTGCTGTCATCTGTCATCTGTCATCTGTCATCTGTCG 364
QY 805 GTTCTCTCTGCTCGTATGTCCTCTGTCATCTGTCATCTGTCATCTGTCATCTGTCG 864
Db 365 TGTAGGATGAG 424
QY 865 TGCCCCAGTAAAAA-AA-AGT-ACAAGGCCATCGGGCTCAATTTTGTGTCATCATCGCGGTG 921
Db 425 TACTTCTCTCTGAGTCCCTACAA 450
QY 922 TTTTTCATTTCTGGACACCTCTACAA 947


```

QY 1085 CTTTGTGGAGAGAGTTCCGGAAGTACCTGCGCCACTTCTTCCACAGGCACTTGCTCA 1144
Db 180 VTGSSBYBCGVNVAVRTSMKTDSTKMBSDMSRRSRVHYGRNM 226
QY 1145 TGCACCTGGCAGACATACATCCCATCTCTTCTAGTAGAGAGCTGGAA 1191

RESULT 7
LOCUS B84215 469 bp DNA GSS 20-AUG-1998
DEFINITION RPC111-22K6.TV RPC111 Homo sapiens genomic clone R-22K6, genomic
survey sequence.
ACCESSION B84215
NID 92925347
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 469)
AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and
Venter,J.C.
Use of BAC End Sequences for Sequence-Ready Map Building (1998)
JOURNAL Unpublished (1998)
COMMENT Other_GSSs: RPC111-22K6.TP
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadam@tigr.org
For clone availability, please contact Pieter de Jong
(pieterdejong.med.buffalo.edu). Clones may be purchased from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html
Seq primer: T7
Class: BAC ends.
FEATURES
location/Qualifiers
source 1..469
/organism="Homo sapiens"
/notes="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPC111 Human Male BAC Library"
/ab_xref="taxon:9606"
/clone="R-22K6"
/clone_lib="RPC111"
/sex="Male"
/cell_type="Lymphocytes"
BASE COUNT 141 a 103 c 113 g 112 t
ORIGIN
Query Match 3.0%; Score 50; DB 27; Length 469;
Best Local Similarity 65.4%; Pred. No. 7.17e-49;
Matches 106; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
Db 14 ACTGTGAACACACAGTCACTGACCAAGCAGGAGGTGACAGAGCTCTTGGGATGA 73
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 995 ACTGTAGCGGAGGAGCATCTGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1054
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 74 CTCACCTGCTGCATCACTCCATCATCTATCGCTTGGGGAGAGTTTCAGAGGTATC 133
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1055 CCCACTCTGCTGAACCCCGGTGATCTACCGCTTTGTTGGAGAGAGGTTCCGGAAGTACC 1114
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 134 TCTCGGTGTTCTTCCGAAAGCAGCATACCAAGGCGCTTCTGCA 175
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1115 TGGCCACTTCTTCCACAGGCACTTGCTCATGCACCTGGGCA 1156
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
RESULT 8
LOCUS AA754458 247 bp mRNA EST 20-JAN-1998
DEFINITION 97SN1784 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa
CDNA clone 97SN1784, mRNA sequence.
ACCESSION AA754458

```

```

NID 92801164
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM rice.
Eukaryota; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
Poales; Poaceae; Oryza.
REFERENCE 1 (bases 1 to 247)
AUTHORS Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R., Moon,E.P.,
Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,
Lee,M.C. and Eun,M.Y.
Large-scale Sequencing Analysis of ESTs from Rice Immature Seed
Unpublished (1998)
COMMENT Contact: Eun M.Y.
Department of Cytogenetics
National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyunggi-do, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
Email: myeun@sun20.astli.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bnhahm@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
FEATURES
location/Qualifiers
source 1..247
/organism="Oryza sativa"
/cultivar="Milyang23"
/notes="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Directional cDNA library inserted into lambda ZAPII
vector at 5' end with EcoRI and 3' end with Xho I site."
/db_xref="taxon:4530"
/clone="97SN1784"
/tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
BASE COUNT 7 a 16 c 21 g 34 t 169 others
ORIGIN
Query Match 2.8%; Score 48; DB 12; Length 247;
Best Local Similarity 13.0%; Pred. No. 4.78e-45;
Matches 29; Conservative 102; Mismatches 90; Indels 2; Gaps 2;
Db 16 CBAMNKHMTBWBCCVRRVGTGTTNNKNGHRTTWNDCSDNAHCRVTVBMYARSKY 75
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Cp 1018 CCAGATGCTTCGTCGCTCACATGTCATT-TCCAAATAAGATGATGATGAGAGAGA 960
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 76 GYGTBYSHNVDTNTGGTGVGKTTVNVHSGWNNRCSNVVYVWBTAYCDYBHYDBRANH 135
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
Cp 959 AGGATAGCCACATTTAGGGTGTCCAGAAATGAAACACCCCATGATGACAAAATG 900
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 136 DTRCTNDRGYN-TASDNGTSATKRTVGYDKTSDCGGCGKRVTYGSSBYBRCGVNV 194
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Cp 899 AGCCGATGCGCTTGATCTATCTTTTCTACGGGACCTCAGCAGCGCTTTGATGATCT 840
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 195 MYRTTSMWTDKTKBMSMDMSRRSRVHYGRWMBNKRGRMSRNW 237
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
Cp 839 GTGTACGATGCGCCATACGAGCAGGAGGAGGAGCAGAGACAGACAGA 797
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
RESULT 9
LOCUS AF034173 2275 bp mRNA EST 22-DEC-1997
DEFINITION Homo sapiens ntcon2 contig mRNA, partial sequence.
ACCESSION AF034173
NID 92707735
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2275)
AUTHORS Tripodis,N. and Ragoussis,J.

```


BASE COUNT	116 a	121 c	105 g	111 t	3 others
ORIGIN					
Query Match	2.1%; Score 36; DB 25; Length 456;				
Best Local Similarity	61.1%; Pred. NO. 2.50e-23;				
Matches	96; Conservative 0; Mismatches 61; Indels 0; Gaps 0;				
Db	186	TGCCACCATCTACTCCATCATCTTCTTAACATGGCATCTGTGGGCAATGGATTTGCTATCC	245		
Qy	290	TGCCCCGGCTGTACTCCCTGGTGTTACATGTGGGCTCTTGGGCAATCTGGTGGTGGA	349		
Db	246	TGCTCATGGGTTACAGAGAAACTGAGAGATCATCGGACAAAGTACAGGCTGCACCTGT	305		
Qy	350	TGATCCTCATAAATACAGAGGCTCCGAATTATGACCAACATCTACCTGCTCAACCTGG	409		
Db	306	CAGTGGCCGACCTCCTCTTTNTTCATCACGCTTCCCTT	342		
	410	CCATTTGGGACCTGCCTCTTCCTCGTCACCCCTTCCATT	446		

RESULT	12				
LOCUS	FR0019847	553 bp	DNA	GSS	10-DEC-1997
DEFINITION	F.rubripes GSS sequence, clone 036L10aA4, genomic survey sequence.				
ACCESSION	AL012734				
NID	92679102				
KEYWORDS	GSS; genome survey sequence.				

SOURCE	Fugu rubripes.
ORGANISM	Fugu rubripes
	Eukaryotae; Metazoa; Chordata; Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Fugu.
REFERENCE	1 (bases 1 to 553)
AUTHORS	Elgar, G., Clark, M., Smith, S., Meek, S., Warner, S., Umrania, Y., Williams, G. and Brenner, S.
TITLE	Direct Submission
JOURNAL	Submitted (08-DEC-1997) MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hgmrc.ac.uk
COMMENT	Vector: pBluescript II KS V_type: phagemid PRIMER: KS DESCR: One pass dye-terminator sequencing of cosmid cloned genomic sequence.

```

sequence, Location/Qualifiers
1..553
  /organism="Fugu rubripes"
  /db_xref="taxon:31033"
  /clone_lib="cosmid 036L10"
  /clone="036L10A4"
BASE COUNT      108 a  157 c  136 g  144 t  18 others

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Query Match      2.1%; Score 35; DB 26; Length 553;
Best Local Similarity 70.7%; pred. No. 1.22e-21;
Matches      58; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
```

Db 331 GAAGCGTGCANAGCACCACATCTACCTGACTCACCTGGCGTGCGGACCTCCTCTT 390
||| ||| | ||| ||||||||| ||||||| | ||||||| |||||
Oy 369 GAGGCTCGGAATTATGACCAACATCTACCTGCTCAACCTGGCCATTTCGACACTGCTCTT 428

Db	391	CGGCTTCACCGTCTGTTCTGG	412
Qy	429	CTCTGTCACCGTTCACATTCTGG	450

RESULT	13				
LOCUS	AA177828	529 bp	mrna	EST	16-FEB-1997
DEFINITION	mt07f02.r1 Soares mouse 3DMS				Mus musculus cDNA clone 620379 5'
					similar to TR:G663021 G663021 PROTEINASE ACTIVATED RECEPTOR 2. ; ;
					mrna sequence.
ACCESSION	AA177828				
NID	G1759090				
KEYWORDS	EST.				

SOURCE ORGANISM	REFERENCE
house mouse. Mus musculus	1 (bases 1 to 529)
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	Marra, M., Hallier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Willson, R. and Waterston, R.
	Waterston, R.
	The WashU-HMMI Mouse EST Project
	Unpublished (1996)
	TITLE
	JOURNAL

Contact: Marra M/Mouse EST Project
WashU-HMMI Mouse EST Project
Washington University School
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:381203
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 494.

```

FEATURES
source
1. .529
location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I oligo(dT) primer [5',
TGTACCAATCTGAAGTGGAGCGCGCGCTGTGTGTGTGTGTGTGTGTGT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. RNA
provided by Dr. Bertrand Jordan. Library went through
three rounds of normalization, and was constructed by
Bento Soares and M.Fatima Donaldo."
/db_xref="taxon:10090"
/clone="620379"
/clone_lib="Soares mouse 3NbMS"
/sex="male"
/tissue_type="Spleen"
/dev_stage="4 weeks"
/lab_post="p4108"

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mrna	/lab_host=DHIOB
BASE COUNT	<1..>529
ORIGIN	110 a 168 c 107 g 144 t

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Best Local Similarity 63.2%; Pred. No. 5.66e-20;
Matches 117; Conservative 0; Mismatches 65; Indels 3; Gaps 2;

DB	134	CAACCTGGCCATCGCAGATCTCCTTTTCTGTGTCACACTTGCACATTTAAGATCGCCTACCA	193
QY	402	CAACCTGGCCATTTTCGAGACGCTCTCTTCCTCGTCACCCCTCCCATCTTGATC--C-ACTA	458

Db 194 TCTCAATGGCACAACACTGGGGTATTTGGCGAGGTACAGTCCGGATCACCACGGTTGTTT 253

QY	Db
459	254

Qy	519	TCACACAGGCTTGTCACGCGAGATCTTTTCATAATCCTGCTGACAAATCGACAGGTACCT	578
Db	314	GGCCA	318

Qy	579	GGCCA	583

RESULT 14

LOCUS FR0019844 539 bp DNA GSS 10-DEC-1997
 DEFINITION F.rubripes GSS sequence, clone 036L10aB4, genomic survey sequence.
 ACCESSION AL012731
 NID 92679099
 KEYWORDS GSS: genome survey sequence.
 SOURCE Fugu rubripes.
 ORGANISM Fugu rubripes
 Eukaryotae; Metazoa; Chordata; Vertebrata; Actinopterygii;
 Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
 Tetraodontiformes; Tetraodontidae; Tetraodontidae; Fugu.
 REFERENCE 1 (Bases 1 to 539)
 AUTHORS Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrana,Y.,
 Williams,G. and Brenner,S.
 TITLE Direct Submission
 JOURNAL MRC Human Genome Mapping Project Resource
 Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hmp.mrc.ac.uk
 COMMENT vector: pBluescript II KS
 V-type: phagemid
 PRIMER: KS
 DESCR: One pass dye-terminator sequencing of cosmid cloned genomic
 sequence.

RES
 source

Location/Qualifiers
 1. .539
 /organism="Fugu rubripes"
 /db_xref="taxon:31033"
 /clone_lib="cosmid 036L10"
 /clone="036L10aB4"
 BASE COUNT 123 a 155 c 128 g 111 t 22 others
 ORIGIN
 Query Match 2.0%; Score 33; DB 26; Length 539;
 Best Local Similarity 67.1%; Pred. No. 2.48e-18;
 Matches 57; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
 Db 141 GCAGCGGTTCCGGAACTCACCCGATGAAGCGGTACACCGGATTCACNGCGCAGT 200
 ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Cp 1117 GCAGTACTTCGGAACTCTCTCCACAAAGCGGTAGATCACCGGGTTCATGCAGCAGT 1058
 ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 201 GCACAAAGCCACACCTTGGTAC 225
 ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Cp 1057 GGGAGTAGCGGATCACCTCTGTCTAC 1033

RESULT 15
 LOCUS AA511931 602 bp mRNA EST 08-JUL-1997
 DEFINITION vgl7f07.r1 Soares mouse NBMH Mus musculus cDNA clone 861637 5',
 similar to gb:L19315 CHOLECYSTOKININ TYPE A RECEPTOR (HUMAN);, mRNA
 sequence.
 ACCESSION AA511931
 SOURCE 92249785
 EST.
 ORGANISM house mouse.
 Mus musculus
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
 Murinae; Mus.
 REFERENCE 1 (Bases 1 to 602)
 AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
 Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
 Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 Waterston,K.
 TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT

Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of MedicineP
 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information..
 MGI:505725
 Seq primer: -28ml3 rev2 ET from Amersham
 High quality sequence stop: 388.
 Location/Qualifiers

FEATURES
 source

1. .602
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
 was primed with a Not I - oligo(gt) primer [5',
 TGTACCAATCTGAAGTGGAGCGCGCGGAAAGTTTTTTTTTTTTTTT
 3']; double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not
 I and Eco RI sites of the modified pT73 vector. RNA
 provided by Dr. Minoru Ko, Wayne State Univ. Library
 constructed and normalized by Bento Soares and M.Patima
 Bonaldo."
 /db_xref="taxon:10090"
 /clone="861637"
 /clone_lib="Soares mouse NBMH"
 /sex="male"
 /tissue_type="heart"
 /dev_stage="4 weeks"
 /lab_host="DH10B"
 <1. .>602
 mRNA 142 a 164 c 144 g 152 t
 ORIGIN
 Query Match 2.0%; Score 33; DB 7; Length 602;
 Best Local Similarity 64.6%; Pred. No. 2.48e-18;
 Matches 73; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
 Db 324 CTGTACTCTTCATATTCCTTCTCAGTGTCTGTGGGAACACGCTGGTTATCACGCTGCTG 383
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 298 CTGTACTCTCTGGTTCACCTGTGGGCTCTTGGGCAATGTGGTGGTGGTATGATCCTC 357
 ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 384 ATTCGAAACAAGAGGATGCGGACTGTCCACCAACATCTTCTGTGTCCCTGGC 436
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 358 ATAAATACAGGAGGCTCCGAATATGACCAACATCTACCTGCTCAACCTGGC 410

Search completed: Tue Dec 8 23:12:46 1998
 Job time : 4040 secs.

M E R E H (TM)

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ch_nn n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Tue Dec 8 23:13:06 1998: MasPar time 241.51 Seconds
Tabular output not generated. 951.505 Million cell updates/sec
Title: >US-08-963-656-1
Description: (1-1689) from US08963656.seq
Perfect Score: 1688
N.A. Sequence: 1 AATCCTTTTCCTGGCACCTC.....CCCTCTTAATGAAAGCTT 1689
Comp: TTAGGAAGAAGGACCGTGAG.....GGGACGAATTACTTTTCGAA

Scoring table: TABLE default
Gap 6
Nmatch STD : Dbase 0; Query 0
Searched: 188442 seqs, 68026449 bases x 2
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: n-geneseq32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39 40:part40

Statistics: Mean 9.514; Variance 5.518; scale 1.724
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Match	Description	Pred. No.
1	1688	100.0	1689 23 T31334 CC-chemokine receptor	0.00e+00
2	1688	100.0	1689 32 T58783 Human C-C chemokine r	0.00e+00
3	1639	97.1	1915 34 T85162 Human chemokine recep	0.00e+00
4	1637	97.0	5099 38 T93601 Human eosinophil eota	0.00e+00
5	1116	66.1	1116 23 T31336 CC-chemokine receptor	0.00e+00
6	1112	65.9	1193 23 T31335 CC-chemokine receptor	0.00e+00
7	1030	61.0	1071 36 T79096 Human CCKR3 chemokine	0.00e+00
8	424	25.1	1065 33 T86154 Human MIP-1alpha/RANT	4.11e-281
9	424	25.1	1495 11 Q62895 C-C chemokine recepto	4.11e-281
10	424	25.1	2156 34 T90384 Human MIP-1 alpha/RAN	4.11e-281
11	355	21.0	1544 34 T86839 cDNA encoding rat CC	1.24e-230
12	225	13.3	1059 34 T85163 Macaque chemokine rec	2.47e-136
13	222	13.2	1225 39 T76920 DNA encoding human CC	3.54e-134

14 13.2 1255 39 T76919 DNA encoding human CC 3.54e-134
15 13.2 1414 25 T44042 Human G-protein chemo 3.54e-134
16 13.2 1477 37 T90117 cDNA for human CCR5 3.54e-134
17 13.2 3883 34 T85161 Human chemokine recep 3.54e-134
18 10.4 1083 35 T96976 Human monocyte chemoa 1.43e-100
19 175 10.4 1979 15 Q96298 Human monocyte chemoa 1.43e-100
20 169 10.0 2232 15 Q96297 Human monocyte chemoa 2.61e-96
21 152 9.0 792 37 T90116 cDNA for inactive hum 2.75e-84
22 152 9.0 1442 37 T90118 cDNA for inactive hum 2.75e-84
23 152 9.0 1557 39 T99542 Human chemokine recep 2.75e-84
24 123 7.3 1607 23 T35277 Chemokine receptor K5 5.55e-64
25 76 4.5 1586 26 T44099 Human G-protein recep 5.47e-32
26 69 4.1 1900 11 Q66162 Partial coding sequen 2.18e-27
27 69 4.1 2058 11 Q66153 Putative seven transm 2.18e-27
28 69 4.1 2154 11 Q64125 Epstein Barr virus in 2.18e-27
29 69 4.1 2160 11 Q66160 Putative seven transm 2.18e-27
30 65 3.9 2751 11 Q66164 Seven transmembrane r 8.68e-25
31 60 3.6 1162 11 Q66170 Seven transmembrane r 1.42e-21
32 60 3.6 2254 11 Q66167 Seven transmembrane r 1.42e-21
33 55 3.3 1119 40 V15418 Human dendritic cell 2.09e-18
34 53 3.1 1373 17 Q99951 Recombinant high affi 3.75e-17
35 51 3.0 1316 39 T99953 Human chemokine recep 6.57e-16
36 51 3.0 1547 40 V15419 Human macrophage/dend 6.57e-16
37 49 2.9 1200 5 Q30011 Sequence encoding a h 1.13e-14
38 49 2.9 1200 17 Q99949 Recombinant high affi 1.13e-14
39 48 2.8 1176 17 Q99950 Recombinant high affi 4.61e-14
40 48 2.8 1883 17 Q99006 Interleukin 8 recepto 4.61e-14
41 48 2.8 1933 5 Q93505 Interleukin-8 recepto 4.61e-14
42 48 2.8 1933 13 Q80520 Interleukin-8 recepto 4.61e-14
43 44 2.6 514 23 T35278 Chemokine receptor cD 1.22e-11
44 43 2.5 1373 5 Q30013 Sequence encoding a l 4.82e-11
45 43 2.5 1748 17 Q99008 Interleukin 8 recepto 4.82e-11

ALIGNMENTS

RESULT 1
ID T31334 standard; DNA; 1689 BP.
AC T31334.
DT 15-NOV-1996 (first entry)
DE CC-chemokine receptor 3 genomic DNA.
KW CC-chemokine receptor 3; CCK-3; Eos-L2; inhibitor; antisense;
KW antinflammatory; eosinophil; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 181..1248
FT variation /*tag= a
FT /*tag= b
FT /*note= "CKR-3 genomic clone has CG at positions
FT 1007-1008, coding for threonine (ACG) at
FT position 276; a cDNA clone has GC at
FT these positions, coding for serine (AGC)"
FT misc_difference 1291
FT /*tag= c
FT /*note= "base n at position 1291 is not identified
FT in the specification"
PN WO9622371-A2.
PD 25-JUL-1996.
PR 19-JAN-1995; U00608.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
PA (CHIL-) CHILDRENS MEDICAL CENT.
PA (LEUK-) LEUKOSITE INC.
PI Gerard CJ, Gerard NP, Mackay CR, Ponath PD, Post TW;
PI Qin S;
DR WPI: 96-354528/35.
DR P-PSDB: W03376.
PT Mammalian chemokine receptor-3 and related nucleic acids - useful to
PT identify receptor inhibitors to treat inflammatory disease, e.g.
PT autoimmune disorders, certain cancers, etc.
PS Claim 1: Page 109: 153pp; English.
CC A genomic DNA clone (T31334) codes for a novel receptor (W03376),


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|||||
QY 420 CTGCTCTCTCGTCCACCTTCACATCTCGATCCACATATGTCAGGGGCAATACTGGGT 479
Db 3886 ttttgccatggtatgtgaagctctctcaggggttttatcacacaggtgtgacagga 3945
QY 480 TTTTGGCCATGGCATGTGAAGCTCCTCTCAGGGTTTATCACACAGGCTTGTACAGGA 539
Db 3946 gatcttttcaatactctgagacaatcgacaggtacatcgccattgtccatgtgttt 4005
QY 540 GATCTTTTTCATATCCCTGCTGACAATCGACAGGTACCTGGCCATTGTCCATGCTGTGT 599
Db 4006 tgccttcgagccggactgtcaacttttggtgtcataccagcatgctcacctggggcct 4065
QY 600 TGCCCTTCGAGCCGGAGCTGTCACTTTTGGTGTATCATCACAGCATGTCACCTGGGGCCT 659
Db 4066 ggcagtgctagcagctcttcctgaatttatctctatgagactgaagagttgtttgaaga 4125
QY 660 GGCAGTGTAGCAGCTCTCTGTAATTTATCTCTATGAGACTGAAGAGTTGTTGAAGA 719
Db 4126 gactcttgagtgctctttaccagagagatacagtatagctggaggaattttccacac 4185
QY 720 GACTCTTTTGCAGTGTCTTTTACCAGAGGATACAGTATATAGCTGGAGGCATTTCCACAC 779
Db 4186 tctgagaatgaccatctctctgctctcctctcctctgctctgttatggccatctgctcac 4245
QY 780 TCTGAGATGACCATCTCTCTGCTCTGCTCTCCCTGCTCTGTTATGGCCATCTGCTACAC 839
Db 4246 aggaatcatcaaacgctgctgaggtgccccagtaaaaaaagtacaggccatccggct 4305
QY 840 AGGAATCATCAAAAGCTGCTGAGGTGCCCGCAGTAAAAAAGTACAAAGGCCATCCGGCT 899
Db 4306 catctttgtcatatggcggtgtttttcaattttcttgacacccctacaatgtggctatcct 4365
QY 900 CATTTTCTCATATGCGCGGTGTTTTTCATTTCTGGACACCCCTACATGTGGGTATCCT 959
Db 4366 tctctctctcatcaatccatctatttggaatgactgtgagcgagcaagcatctgga 4425
QY 960 TCTCTTCTCATCAATCCATCTTATTGGAATGACTGTGAGCGGACGAAGCATCTGGA 1019
Db 4426 cctggtcatgtgtgacagaggtgatgcctactcccactgtcgtgcatgaacccgggtgat 4485
QY 1020 CTGTGTATCTGTGTGACAGAGGTGATCGCCTACTCCACTGCTGTCATGAACCCGGTGAT 1079
Db 4486 ctacgctttttgagagaggttccggaagtactcgtgcgaacttttccacaggaactt 4545
QY 1080 CTACGCCCTTTTGGAGAGAGGTTCCGGAAGTACTGTGCGCACTTCTTCCACAGGCATT 1139
Db 4546 gctcatgacctgggcagatcacatccattctctcttagtgagaagctggaagaacacag 4605
QY 1140 GCTCATGCACTGGGCAGATACATCCCATTCCTCTTAGTGAGAGCTGGAAGAACCCAG 1199
Db 4606 ctctgtctctccatccacagcagagccgggaactctctattgttttaggtcagatgcag 4665
QY 1200 CTCGTCTCTCCATCCACAGCAGAGCGGAACTCTCTATTGTGTTTAGGT-AGATGCAG 1258
Db 4666 aaaattgctaaagaggaagaccaaagagatgaagcaaacacatttaagccttccacact 4725
QY 1259 AAAATTGCTTAAAGAGGAAGGACCAAGAGATNAAGCAAAACACATTAAAGCCTTCCACT 1318
Db 4726 cactctaaaaacagctcttcaaac-ttccagtgaacactgaagctcttgaagacactga 4784
QY 1319 CACTCTAAAACAGTCTTCAAACTTCCAGTGAACACTGAAAGCTCTT-AAGACACTGA 1377
Db 4785 aatacacacagcagtagcagtagatgcatgtacccttaaggtcattaccacagggcagg 4844
QY 1378 AATATACACAGCAGTAGCAGTAGATGATGATACCCCTAAGCTCATTACACAGGCCAGG 1437
Db 4845 ggcctgggagcgtagctactatacaacccttaaaagcagaggtttgtctctctctaaaa 4904
QY 1438 G-CTGGGAGCGGTACTCATCATCAACC-TAAAAAGCAGAGCTTTGCTTCTCTCTAAAA 1495
Db 4905 tgagtactcactacatttaagtgcactgaatgttagatgtagttactatgctcgctacaaaa 4964
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QY 1496 TGAGTTACCTATATTTTAAATGCACCTGAATGTTAGATAGTTACTATATCGCGCTACAAA 1555
Db 4965 agtataactttttatatatttatataacttaacttcagcagctatttgataataaaca 5024
QY 1556 AGGTAAACATTTTATATTTTATACATTAACCTCAGCCAGCTATT-ATATAAATAAACA 1614
Db 5025 ttttcacacaataaagaatgaactattttatttttaataatgctagttcttccctg 5084
QY 1615 TTTTCACACAAATCAATAAGTTAACTATTTTATTTTAAATGCGCTAGTCTTTCCTCG 1674
Db 5085 cttaaatgaaaagctt 5099
QY 1675 CTTAATGAAAAGCTT 1689

RESULT 5
ID T31336 standard; DNA; 1116 BP.
AC T31336;
DT 13-NOV-1996 (first entry)
DE CC-chemokine receptor 3 consensus DNA sequence.
KW CC-chemokine receptor 3; CKP-3; Eos-L2; inhibitor; antisense;
KW antiinflammatory; eosinophil; ds.
OS Homo sapiens.
PN W0962371-A2.
PD 23-JUL-1996.
PF 19-JAN-1996; U00608.
PR 19-JAN-1995; US-375199.
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.
PA (CHIL-) CHILDRENS MEDICAL CENT.
PA (LEUK-) LEUKOSITE INC.
PI Gerard CJ, Gerard NP, Mackay CR, Ponath PD, Post TW;
PI Qin S;
PI WPI; 96-354528/35.
DR P-PSDB; W03378.
PT Mammalian chemokine receptor-3 and related nucleic acids - useful to
PT identify receptor inhibitors to treat inflammatory disease, e.g.
PT autoimmune disorders, certain cancers, etc.
PS Claim 1; Page 114-115; 153pp; English.
CC A consensus DNA sequence (T31336) codes for a novel human receptor
CC (W03378), designated Eos L2 or C-C chemokine receptor 2 (CKR-3).
CC It was deduced by comparing a genomic clone (T31334) and a cDNA
CC clone (T31335) coding for CKR-3 proteins (W03376 and W03377) having
CC slightly different sequences. Initial sequence information revealed
CC 2 regions in which the cDNA sequence appeared to be shifted in
CC frame, resulting in 2 sets of 4 contiguous amino acid differences
CC in the predicted proteins. Further sequence analysis revealed only
CC a single difference between the 2 open reading frames, the genomic
CC clone coding for threonine at position 276 and the cDNA clone for
CC serine.
SQ Sequence 1116 BP; 246 A; 286 C; 257 G; 306 T;

Query Match. 66.1%; Score 1116; DB 23; Length 1116;
Best Local Similarity 98.1%; Pred. No. 0.00e+00;
Matches 1095; Conservative 21; Mismatches 0; Indels 0; Gaps 0;

Db 1 cagggagaagtgaatgacaacctcactacatagatcacagtttgagacctttgttaccacatcct 60
QY 167 CAGGGAGAAGTGAATGACAACCTCACTAGATACAGTTGAGACCTTTGGTACCACATCCT 226
Db 61 actatgatgcgtgggcctctctctgtgaaaaaagctgtataccagagactgatggccagt 120
QY 227 ACTATGATGACGTGGGCGCTCTCTGTGAAAAGCTGTATACCAGAGCACTGATGGCCAGT 286
Db 121 ttgtgccccgcgtactcctcctggtgttactgtggcctcttgggcaatgtggtgtg 180
QY 287 TTGTGCCCCGCGTGTACTCCTCTGTTGTTCACTGTGSCCTTCTTGGGCAATGTGGTGTGG 346
Db 181 tgatgatctctataataacacagaggtctccgaattatgaccaacatctacctgtcaacc 240
QY 347 TGATGATCTCTATAAATAACAGGAGGCTCGGAATTATGACCAACATCTACCTGCTCAACC 406
Db 241 tggccatttcggacgctctctctctgtacccttcattctgattccatctatgtcagg 300
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QY 407 TGGCCATTTCGGACCTGCTCTTCCTCGTCACACCTTCCCAATCTTGATCCACTATGTCAGGG 466
Db 301 ggcataactgggtttttggccatgcatgtgtaagctctctcagggttttatcacacag 360
QY 467 GGCATAACTGGGTTTTTGGCCATGCAATGTGAAGCTCTCTCAGGGTTTTATCACACAG 526
Db 361 gctgtacagcagatctttttcataaactcgtctgacaaatcacacaggtacacctggccattg 420
QY 527 GCTGTACAGCCAGATCTTTTCATAATCTGCTGACATCCACAGGACCTGGCCATTG 586
Db 421 tccatgctgtgttggcccttcgagccggactgttcaacttttgggttcacaccagcatcg 480
QY 587 TCCATGCTGTGTTGGCCTTCGAGCCGAGCTGTACATTTTGGTGTCAATCACCAGCATCG 646
Db 481 tcaactgggctggcagctgtagcagctcttctcgaatttatcttctatgagactgaag 540
QY 647 TCACCTGGGGCTGGCAGTGTAGCAGCTTTCCTGAAATTTATCTTCTATGAGACTGAAG 706
Db 541 agtgtttgaagagactmttttcagctgcttttaccagagagatcacagtatatagctgga 600
QY 707 AGTTGTTGAAGAGACTCTTTCGAGTGTCTTTACCAGAGGATACAGTATATAGCTGA 766
Db 601 gssattccacacttgagaatgacatcttctgtctcttccctctgctgctgtatgg 660
QY 767 GGCATTTCCACACTCTGAGAATGACATCTTCTGCTCTGCTTCCCTCTGCTGCTTATGG 826
Db 661 ccatctgtcacaggaatcataaagcgtcgtgaggtgccccagtaaaaaaaagtaca 720
QY 827 CCATCTGCTFACACAGGAATCATCAAAACCTGCTGAGGTGCCCCAGTAAAAAAGTACA 886
Db 721 aggcacatccggtcattttgttcacatcagcggtgtttttcatttcttgacacccctaca 780
QY 887 AGCCATCCGGCTCATTTTGTTCATCATCGCGGTGTTTTTCATTTCTGGACACCCCTACA 946
Db 781 atgtggctatccttctctctctscymwmywycatcttatttggaaatgactgtgagcggm 840
QY 947 ATGTGCTATCTTCTCTCTTCTATCAATCATCTTATTTGGAAATGACTGTGAGCGGA 1006
Db 841 mgarismwykgacacttgctcgtgtgtgagagaggttccggaagtacacctgcccacttst 960
QY 1007 CGAAGCATCTGACCTGGTCATGCTGGTGACAGAGGTGATCGCCTACTCCCACTGCTGCA 1066
Db 901 tgaacccggtgactacgccttgttggagagaggttccggaagtacacctgcccacttst 960
QY 1067 TGAACCCGGTGATCTACGGCTTTTGTGGAGAGAGGTTCGGAAGTACCTTCCGCCACTTCT 1126
Db 961 tccacagggcacttgcctgcatgcacctgggagatatacatccattccttccctagtgagaagc 1020
QY 1127 TCCACAGGCACCTTGCTCATGCACCTGGGCAGATACATCCCATCTTCTCTAGTGAGAAGC 1186
Db 1021 tggaaagaacccgctctgtctctccatccacagcagagccggaactctctattgtgtttt 1080
QY 1187 TGGAAAGAACCAAGCTGTCTCTCCATCCACAGCAGAGCGGAACTCTCTATTGTGTTTT 1246
Db 1081 agtgatgacacaaaattccctaaagagagagacc 1116
QY 1247 AGGTAGATCAGAAAATTCCTTAAGAGAGGAGACC 1282
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RESULT 6

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ID T31335 standard; cDNA; 1193 BP.
AC T31335;
DT 15-NOV-1996 (first entry)
DE CC-chemokine receptor 3 cDNA clone.
KW CC-chemokine receptor 3; CXR-3; Eos-L2; inhibitor; antisense;
KW antiinflammatory; eosinophil; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 92..1159 /*tag= a
FT variation 918..919 /*tag= b
FT /*note= "CXR-3 cDNA clone has GC at positions
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FT 918-919, coding for serine (AGC) at
FT position 276; a genomic clone has CG at
FT these positions, coding for threonine
FT (AGC)."
PN WO9622371-A2.
PD 25-JUL-1996.
PF 19-JAN-1996; U00608.
PR 19-JAN-1995; US-375199.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
PA (CHIL-) CHILDRENS MEDICAL CENT.
PA (LEUK-) LEUKOSITE INC.
PI Gerard CJ, Gerard NP, Mackay CR, Ponath PD, Post TW,
PI Qin S;
DR WPI: 96-354528/35.
DR P-PSDB; W03377.
DR Mammalian chemokine receptor-3 and related nucleic acids - useful to
PT identify receptor inhibitors to treat inflammatory disease, e.g.
PT autoimmune disorders, certain cancers, etc.
PS Claim 1; Page 11-113; 153pp; English.
CC A genomic DNA clone (T31335) codes for a novel receptor (W03377),
CC designated Eos L2 or C-C chemokine receptor 3 (CXR-3), involved
CC in leukocyte migration associated with inflammation. It was
CC isolated from a human library constructed from eosinophils obtd.
CC from a patient with hyper-eosinophilic syndrome using a probe
CC (p4 cDNA) encoding the MIP-lalpha/RANTES receptor. A CXR-3
CC genomic clone (T31334) was also isolated, and a consensus sequence
CC is given in T31336. The cDNA and genomic clones can be used for
CC the prodn. of recombinant CXR-3 in host cells, or to design
CC antisense sequences useful for treating inflammatory disease.
SQ Sequence 1193 BP; 274 A; 310 C; 275 G; 334 T;
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Query Match 65.9%; Score 1112; DB 23; Length 1193;

Best Local Similarity 99.8%; Pred. No. 0.008+00;

Matches 1114; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 78 caggagagaagtgaatgacaacctcactagatagacagcttgggtaccacatcct 137
QY 167 CAGGAGAGAGTGAATGACACACCTCCTACTAGATACAGTTTGAGACCTTTGGTACCACATCCT 226
Db 138 actatgatcagctgggctcgtctgtgaaaagctgtaccagagcactgatgccccagt 197
QY 227 ACTATGATGACGTGGGCTGCTCTGTGAAAAGCTGTATACCAGAGCACTGATGGCCCACT 286
Db 198 ttgtcccccgctgactccctcgtgttcactgtgggctcttgggcaatgtggtggtgg 257
QY 287 TTGTGCCCCCGCTGTACTCCCTGCTGTGTTCACTGTGGGCTCTTGGGCAATGTGGTGGTGG 346
Db 258 tgatgatcctataaaatcacaggaggtccgaattatgaccaacatcactcgtccaacc 317
QY 347 TGATGATCCTCATANAATACAGAGGCTCCGAATATGACCAACATCTACCTGTCTCAACC 406
Db 318 tggccatttcggacctgctcttctcctcgtcaccccttccattcttgatccactatgccaagg 377
QY 407 TGGCCATTTCGGACCTGCTCTTCTCTCGTCACCTTCCATTTCCGATCCACATGTCAGGG 466
Db 378 ggcataactgggtttttggccatggcagtgtaagctcctctcagggtttttatcacacag 437
QY 467 GGCATAACTGGGTTTTTGGCCATGGCATGTGTAAAGCTCTCTCAGGGTTTTATCACACAG 526
Db 438 gctttacagcagagatctttttcataatcctcgtgacaaatcgacaggtacacctggccattg 497
QY 527 GCTTGTACAGCAGATCTTTTTCATATCTCTGCTGACAAATGACAGGATCTTGGCCATTG 586
Db 498 tccatgctgtgtttggcccttcgagccccgactgtcacttttgggtgtcatcacacagcatcg 557
QY 587 TCCATGCTGTGTTTGGCCCTTCGAGCCCGAGCTGTCTACATTTTGGTGTCTATCACCAGCATCG 646
Db 558 tcaactggggcctggcagtgtagcagctcttctcctgaatttatcttctatgagactgaag 617
QY 647 TCACCTGGGGCTGGCAGTGTAGCAGCTCTCTCTGAAATTTATCTTCTATGAGACTGAAG 706
Db 618 agtttttgaagagactcttttgcagtgctcttaccagagagatagatatagctgga 677
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Db 159 cctggtgctcctgctcctgtgcaatacaagagggtataaaacacatgaccagcatctact 218
QY 339 GGTGTGTGTGATGCTCTCAATATAATACAGGAGGCTCCGAATTTATGACCAACATCTACT 398
Db 219 cctgaacctggccattctcctgacctctctcctgttcacgcttccctctctgagtcgacta 278
QY 399 GCTCAACCTGGCCATTTCGGACCTGCTCTCTCTGTCACCTTCCATTTCTGGATCCACTA 458
Db 279 caagttgaagggatgactgggttttgggtgagccatggtgtaagatccctctctggtttta 338
QY 459 TGTGAGGGGGCAATAACTGGGTTTTTGGGCATGGCATGTGTAGCTCTCTCAGGGTTTTA 518
Db 339 ttacacaggtctgacagagagatcttttcaatcactcctgctgacagattgacaggtactc 398
QY 519 TCACACAGGCTTGTACAGCGAGATCTTTTCAATATCTGCTGACAAATCGACAGGTACT 578
Db 399 ggcctcgtccacgcgctgttggcttggggcgcagcgacctcacttttgggtggtcatcac 458
QY 579 GGCCATTGTCATGTGTGTTGGCCTTCGAGCCCGGACTGTCATTTTGGTGTGTCATCAC 638
Db 459 cagcatcatcttggggccctggccatcttgggttcccatgcccagggcttatacttttccaa 518
QY 639 CAGCATGCTGCTACCTGGGCTGGCAGTGTAGCAGCTCTCTCTGAATTTATCTTCTATGA 698
Db 519 gacccaatgggaattcaactcaacacacacctgacgcttcaacttctcactcgaagacctacg 578
QY 699 GACTCAAGAGTTGTTGAAGAGACACTTTTGCAGTCTCTTTACCCAGAGGATACAGTATA 758
Db 579 agagtggagctgttccaggtctgaactgaactccttgggtggtatgctcttgggtttgt 638
QY 759 TAGCTGGAGGCAATTTCCACACTCTGAGATGACCAATCTCTGCTCTCTCTCTCTCTCT 818
Db 639 ggtcatgatcatctgctacacagggattataaagattctgctaagacgacccaatagaa 698
QY 819 CTTTATGTCATCTCTACACAGGAATCATCAAAAGCTGCTGAGGTGCCCGAGTAAAAA 878
Db 699 gaaatccaaagctgctcgttggatttggatcactatgatcacttcttctctcttctgac 758
QY 879 AAAGTACAAAGGCCATCTGGACCTGGTATGCTGTCATCATGCGGTGTTTTTCATTTCTGAC 938
Db 759 cccctacaattgactatactattctgttttccaaagactcctgttccacccatgagt 818
QY 939 ACCCTACATGCTGCTATCT 998
Db 819 tgagcagagcagacatttggacctggctgcaagtgcagggaggtgactgctcactacgca 878
QY 999 TGAGCGGACGAAGCATCTGGACCTGGTATGCTGCTGACAGAGGTGATCGCTACTCCCA 1058
Db 879 ctgctgtgtcaaccagtgatcagccttctggtgagaggttccggaagtaactgcg 938
QY 1059 CTGCTGTCATGAACCCGGTGTATCTAGCCCTTTTGTGGAGAGAGGTTCCGGAAGTACTCGC 1118
Db 939 gcagttgtccacagcggtgtgctgtgacactgttataatggctccctctcctcctcgt 998
QY 1119 CCACCTTCTCCACAGGCACTGCTCATGACCTGGGAGATACATCCCATCTCTCTCTCT 1178
Db 999 ggacaggtgtgagaggttcagctccacatctcctccacaggggagcagtaactctgc 1058
QY 1179 TGAGAAGCTGGAAGAACACAGCTCTGCTCTCTCTCCATCCACAGCAGAGCCGGAACCTCTCTAT 1238
Db 1059 tgggtt 1064
QY 1239 TGTGTT 1244

RESULT 10

ID T90384 standard; DNA; 2156 BP.
AC T90384;
DT 21-JAN-1998 (first entry)
DE Human MIP-1 alpha/RANTES receptor gene.
KW Macrophage inflammatory protein-1 alpha; MIP-1 alpha;
KW reduced upon activation normal T expressed and secreted; RANTES;

KW receptor; cytokine; antiinflammatory; inflammation; human; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 63..1130 /*tag= a
PN US5652133-A.
PD 29-JUL-1997.
PF 28-JAN-1993; 012988.
PR 28-JAN-1993; US-012988.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PI Murphy PM;
DR WPI: 97-392945/36.
DR P-PSDB: W26588.
PT MIP-1 alpha and RANTES receptor nucleic acid - used to develop
PT products for the detection of these cytokine(s) and their receptors,
PT particularly in inflammatory processes
PS Claim 1; Column 11-16; 12pp; English.
CC This nucleic acid sequence encodes a claimed receptor for macrophage
CC inflammatory protein-1 alpha (MIP-1 alpha) and regulated upon
CC activation normal T expressed and secreted (RANTES) protein. Also
CC claimed are: (1) a subsequence of the nucleic acid, having at least
CC 12 contiguous nucleotides; (2) a cell transformed or transfected
CC with the nucleic acid; and (3) purified MIP-1 alpha/RANTES receptor
CC polypeptide. The products can be used for detecting the MIP-1
CC alpha/RANTES receptor and polymorphisms in physiological samples.
CC In addition, the receptor can be expressed and used to assay for
CC MIP-1 alpha/RANTES in biological samples. The quantitation of MIP-1
CC alpha/RANTES is useful for monitoring the levels of these cytokines
CC in a patient. Such measurements are useful in following the anti-
CC inflammatory effects of drugs and prospective usefulness of new anti-
CC inflammatory agents.
SQ Sequence 2156 BP; 538 A; 547 C; 504 G; 567 T;

Query Match 25.1%; Score 424; DB 34; Length 2156;
Best Local Similarity 71.9%; Pred. No. 4, 11e-281;
Matches 695; Conservative 0; Mismatches 271; Indels 0; Gaps 0;
Db 161 ggcacaaactgtgcccctcctgtactcctgtgtatctgtcattggcctggttgaaacat 220
QY 279 GCGCAGCTTTGTCGCCCGCTGTACTCCTGCTGCTACTGCTGGCCCTCTTGGGCAATGT 338
Db 221 cctggtgctcctgtcctgtgcaatacaagagcttaaaacacatgaccagcatctactc 280
QY 339 GGTGTGTGTGATGCTCTCAATATAATACAGGAGGCTCCGAATTTATGACCAACATCTACT 398
Db 281 cctgaacctggccatttctgacctgctctcctgtgttcaacgcttccctctgagtcgacta 340
QY 399 GCTCAACCTGGCCATTTCGGACCTGCTCTCTCTGTCACCTTCCATTTCTGGATCCACTA 458
Db 341 caagttgaagggatgactgggttttgggtgagccatggtgtaagatcctctctggtttta 400
QY 459 TGTGAGGGGGCAATAACTGGGTTTTTGGCCATGGCATGTGTAGCTCTCTCAGGGTTTTA 518
Db 401 ttacacaggtctgacagagatcttttcaatcactcctgctgacagattgacaggtactc 460
QY 519 TCACACAGGCTTGTACAGCGAGATCTTTTCAATATCTGCTGACAAATCGACAGGTACT 578
Db 461 ggcctcgtccacgcggtgttggcttggggcgcagcgacctcacttttgggtggtcatcac 520
QY 579 GGCCATTGTCATGTGTGTTGGCCTTCGAGCCCGGACTGTCATTTTGGTGTGTCATCAC 638
Db 521 cagcatcatctattgggcccctggccatcttgggttccatgcccaggttatactttccaa 580
QY 639 CAGCATGCTCACCCTGGGCGCTGGCAGTGTGCTAGCAGCTCTCTCTGAATTTATCTTCTATGA 698
Db 581 gacccaatgggaattcaactcaacacacctgacgcttcaacttctcactcagcaagacctacg 640
QY 699 GACTGAGAGAGTTGTTGAAGAGACTCTTTTTCAGCTGCTCTTTTACCCAGAGGATACAGTATA 758
Db 641 agagtggagctgttctcaggtctgaaactgaactccttgggtggttattgctcttgggt 700
QY 759 TAGCTGGAGGCAATTTCCACACTCTGAGATGACCAATCTCTGCTCTCTCTCTCTCTCT 818

[illegible]

```

RESULT 11
ID T96839 standard; cDNA; 1544 BP.
AC T86839;
DE 19-DEC-1997 (first entry)
DE cDNA encoding rat CC chemokine receptor.
KW rat; CC chemokine receptor; screen; binding; ligand; ds.
OS Rattus rattus.
FH Key Location/Qualifiers
cds 33..1100
FT /*tag= a
FT PN J09237599-A.
FT PD 02-SEP-1997.
FT PD 22-FEB-1996; 035192.
FT PD 22-FEB-1996; JP-035192.
PA (TAKE ) TAKEDA CHEM IND LTD.
DR WPI; 97-486426/45.
DR P-PSDB; W29179.
DR CC chemokine receptor protein - useful to screen for novel binding
PT compounds
PT Claim 4; Page 21-22; 26pp; Japanese.
PS CC This cDNA encodes a rat CC chemokine receptor. The receptor can be used
CC to screen for novel binding compounds and for preparation of antibodies
CC or antiserum.
SQ Sequence 1544 BP; 415 A; 347 C; 330 G; 452 T;

```

Query Match 21.0%; Score 355; DB 34; Length 1544;
Best Local Similarity 68.1%; Pred. No. 1.24e-230;
Matches 609; Conservative 0; Mismatches 314; Indels 0; Gaps 0;

[illegible]

Db	286	tcacttacccttctcggattgactacaagctgaagacaacactggtttttgggtgatgccca	345
QY	434	TCACCCCTCCATCTCGGATCCACTATGTACAGGGGCATAACTGGGTTTTTGGCCATGGCA	493
Db	346	tgtgtaagcttctctcgtggttttattaccctggccttatcacagtgaagatctctttatca	405
QY	494	TGTGTAAAGCTCTCTCAGGGTTTTATCACACAGGCTGTGTACAGCGAGATCTTTTTTCATAA	553
Db	406	tccctgctgacaattgacaggttacctggccattgtccatgcagtgtttccctgagggccc	465
QY	554	TCTCTGTGACANTGCACAGGTACCTTGCCATTGTCCATGCTGTGTTGCCCTTCGAGCC	613
Db	466	gaactgcaacttttggcgcatacaccagdtattattttggccctcagccatcttagctt	525
QY	614	GGACTGTCACTTTTGGTGTGTCATCACACAGCATGTCACCTGGGGCTGGCAGTGTACAG	673
Db	526	ctattcctgcctatgctttttccaagggccagtgaggagttcactcacaccatcctgtagcc	585
QY	674	CTCTTCTCAATTTATCTTCTATGAGACTGAAAGTGTGTTTGAGAGACATCTTTTGCAGTG	733
Db	586	ctcatttccccgatgagagcctgaagacgctggaagaggtttcaggcctctaaagctaaacc	645
QY	734	CTCTTTACCCAGAGGATACAGTATATAGCTGGAGGCATTTCCACACTCTGAGATGACCA	793
Db	646	tccttggactaatttaccctctgttagtcatgataatttgctacgcaggggatacatcaaaa	705
QY	794	TCPTCTGTCTCGTCTTCCTCTGCTGCTGTATGGCCATCTGTCACAGGAATCATCAAAA	853
Db	706	tctgctcagacgacccaatgagagaagagggaagccgctgcctgatatttgcattta	765
QY	854	CGTGTCTGAGGTGCCCGCAGTAAAAAAGTACAGGCCATCCGGCTCATTTTGTCTATCA	913
Db	766	cgcttctattcttcctctgagcccccctacaatctgaactgtatttgttctgctttcc	825
QY	914	TGGCGGTGTTTTTCATTTTCTGGACACCCTACAATGTGGCTATCCTCTCTCTTCCCTATC	973
Db	826	aagatgttctattaccacaatcagttgtgacgagagcaagcagctggacctggccatacagg	885
QY	974	AATCCATCTATTATGGAAATGACTGTGACGACGAAGCATCTGGACCTGGTCACTGCTGG	1033
Db	886	tgactgaagtgttgctcacaccactgtgtgtcaatccaatcatattatgtctttgttg	945
QY	1034	TGACAGAGTGATCGCTACTCCCACTGCTGCATGAACCCGGTGATCTACGCCTTTGTG	1093
Db	946	gtagcgggttcgggaagtacccttcgggcagctgtttccaagagcatgtggctataccgctgg	1005
QY	1094	GAGAGAGGTTCGGAGTAGTACCTGCGCCACTTCTTCTCCACAGGCACATTGCTCATGCACTGG	1153
Db	1006	cagaaatggctgccccttctctctgtgtggaccactagaagaccaggttcccttaactccat	1065
QY	1154	GCAGATACATCCCATTCCTTCTCTAGTGAGAGCTGGAAAGAACACAGCTCTGCTCTCCAT	1213
Db	1066	ccacaggagaacatgaactttct	1088
QY	1214	CCACAGCAGAGCGCGAACTCTCT	1236

RESULT	12	
ID	T85163	standard; cDNA; 1059 BP.
AC	T85163	
DT	14-DEC-1997	(first entry)
DE	Macaque chemokine receptor 88C.	
KW	Chemokine receptor 88C; atherosclerosis; tumor; asthma; viral infection; autoimmune disease; therapy; drug protein coupled receptor; ss.	
KW	tumor; asthma; viral infection; autoimmune disease; therapy; drug protein coupled receptor; ss.	
QS	Macaca sp.	
PN	W09727698-A2.	
PD	26-JUN-1997.	
PF	20-DEC-1996; U20759.	
PR	07-JUN-1996; US-661393.	
PR	20-DEC-1995; US-575967.	

DE macaque chemokine receptor 8b.
 KW Chemokine receptor 8b; atherosclerosis; rheumatoid arthritis;
 KW tumour; asthma; viral infection; AIDS; inflammation;
 KW autoimmune disease; therapy; diagnosis; leukocyte trafficking;
 KW G protein coupled receptor; ss.

Db	303	c--agtgggactttggaatacaaatggtcaactcttgacagggctctatttttaggct	360
Qy	470	ATAACTGGGTGTTTTGGCCATGGCAATGTGTAAGCTCCTCTCAGGGTTTTATCACACAGGCT	529
Db	361	tcctctcgaactctcttcacatctctctcgaatcgataggtacctggctctctctcc	420
Qy	530	TGTACAGGAGATCTTTTTTCATAACTCTGCTGACAAATCGACAGGTACTGCGCCATTGTCC	589
Db	421	atgctgtgtttgctttaaaagccaggacggtcacctcttggggtggatgacagtgtgatca	480
Qy	590	ATGCTGTGTTGGCCCTCGAGCCGGGACATGTCACATTTGGTGTATCACACGATCGTCA	649
Db	481	cttgggtggtgggtgtgttggogtctctccccagggaatcatctttaccagatctctcaaaag	540
Qy	650	CCTGGGCCCTGGCAGTGTCTAGCAGCTCTTCCCTGGAATTAATCTCTATGAGACTGAAGAGT	709
Db	541	aaggcttcattcacactcgactcagctctcatctttccatacagt-cagtatcaattctggaag	599
Qy	710	TGTTTGAAGAGACTCTTTGCAGTGTCTTTATCCCGAGGATACAGTATATAG-CTGGAGG	768
Db	600	aattccagacattaaagatagtcattcttgggctggctgcgcctgctgtctcatgtctc	659
Qy	769	CATTTCACACTCTGAGAATGACCATCTTCTGCTCGTTCTCCCTCTGCTGTTATGSCC	828
Db	560	atctgctactcgggaatcctctaaaacctctgctctcggtgtcgaaatcgagaagaagagcgc	719
Qy	829	ATCTGCTACACAGGAATCATCAAAAGCGCTGTGAGGTGCCCGCAGTAAAAA-AA-AGT-AC	885
Db	720	agggcttggggcttatcttcaccatcatgattttatttctctctctgggctccctac	779
Qy	886	ANGGCCATCCGGTCAATTTTGTGCATCATGGCGGTGTTTTTCATTTCTTGACACCCCTAC	945
Db	780	aacattgctctctctcgaacacctccaggaaattctttggcctgaaataattgcagtagc	839
Qy	946	AATGTGGCTATCTCTCTCTCTTCCATATCAATCCATCTTATTTTGGAAATGACTGTGAGCGG	1005
Db	840	tctaaaggttggaaccaagctatgcagggtgacagagactcttggagatgaacgaactgtctgc	899
Qy	1006	ACGAAGCATCTGAGACTTGCTATGCTGGTGGTGCACAGAGGTGATGCCCTACTCCCACTGTCTC	1065
Db	900	ateaaccccatcatctatgctcttctcgggggagaagttcagaataactcctcttagtcttc	959
Qy	1066	ATGAACCCGGTGTATCTACGCCCTTTGTGGAGAGAGGTTCCGGGAAGTACTCTGGCCACTTC	1125
Db	960	ttccaaaagcac	971
Qy	1126	TTCCACAGGCAC	1137

RESULT	14	
ID	T76919	standard; cDNA; 1255 BP.
AC	T76919;	
DT	08-JUN-1998	(first entry)
DE	CC encoding human CC chemokine receptor 5 (CCR5) A127L variant.	
KW	CC chemokine receptor 5; CCR5; G-protein coupled receptor;	
KW	human immunodeficiency virus; HIV; CB4; AIDS; therapy;	
KW	transgenic animal; ss.	
OS	Homo sapiens.	
EH	Key	Location/Qualifiers
FT	CDS	1..1116
FT		/+tag= a
FN	W09745543-A2..	
PD	04-DEC-1997.	
PF	28-MAY-1997; U09586.	
PR	28-MAY-1996; US-018508.	
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.	
PI	Alkhatib G, Berger EA, Broder CC, Combadiere C,	
PI	Feng Y, Kennedy PE, Murphy PM;	
PI	WPI: 98-032650/03.	
DR	P-PSDB: W23834.	
DR	CC chemokine receptor 5 polypeptide - used to inhibit membrane	
PT	fusion between HIV and a target cell	
PT		

PS Claim 15; Fig 1B; 70pp; English.

CC This DNA sequence codes for an Alal27Leu variant (see W23834)

CC of a novel human macrophage-selective CC chemokine receptor (see

CC also W23835) that has been designated CCR5. It was isolated from a

CC lambda gt11 cDNA library. The conservative amino acid substitution

CC should not affect the biological activity of CCR5. The

CC susceptibility of human macrophages to HIV infection depends on

CC cell surface expression of the human CD4 molecule and CCR5. CCR5

CC is a member of the 7-transmembrane superfamily of G-protein

CC coupled cell surface molecules. It plays an essential role in the

CC membrane fusion step of infection by some HIV isolates. The

CC establishment of stable, non-human cell lines and transgenic

CC mammals having cells that coexpress human CD4 and CCR5 provides

CC valuable tools for research of HIV infection. Antibodies that bind

CC to CCR5, CCR5 variants, and CCR5-binding agents capable of blocking

CC membrane fusion between HIV and target cells represent potential

CC anti-HIV therapeutics for macrophage tropic strains of HIV.

CC Antisense oligonucleotides can also be used to inhibit expression

CC of CCR5 in a cell.

CC Sequence 1255 BP: 295 A; 311 C; 289 G; 360 T;

SQ

Query Match 13.2%; Score 222; DB 39; Length 1255;
Best Local Similarity 65.4%; Pred. NO. 3.54e-134;
Matches 557; Conservative 0; Mismatches 287; Indels 8; Gaps 7;

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158			
159			
160	Qy	TGCCCCGCTGTACTCCTCGTGTTCACCTGGGCCCTCTGGGCAATTGGTGGTGTGA	349
161			
162			
163			
164	Db	tcattctgataaactgcaaaagctgaagacatgactgacatctcactcgtctcaacctgg	274
165			
166			
167			
168	Qy	TGATTCCTCATAAATACAGAGGCTCCGAATTATGACCAACTCTACCTGCTCAACCTGG	409
169			
170			
171			
172	Db	ccattctgacctgttttctcttactgtccctctcgttgggtcactactt--ggccgc	332
173			
174			
175			
176	Qy	CCATTTCGGACCTGCTCTCTCGTCACCCCTTCATTCTGGATCCACTATGTCAGGGGC	469
177			
178			
179	Db	ccag-tgggactttggaaatacaatgtgcaactcttgacagggctctattttataggct	391
180			
181			
182	Qy	ATAACTGGGTTTTGGCCATGGCATGTGTAAGCTCTCTCAGGGTTTTATCACACAGGCT	529
183			
184			
185	Db	tcttctctgaaattcttcttcatcctctctcctgcacatcgataggtacctggtctggtcc	451
186			
187			
188	Qy	TGTACACGAGATCTTTTTCATAATCTGCTGCAATCGACAGGTACTTGGCCATTGTCC	589
189			
190			
191	Db	atgctgtgtttgttttaaaacgacagcagctcaccctttgggtgggtgacaagtgtgatca	511
192			
193			
194	Qy	ATGCTGTGTTTGCCCTTCGAGCCGGACTGTCACTTTTGGTGTCATCACCAAGCATCGTCA	649
195			
196			
197	Db	cttgggtggctgctgtgtttgctctctccaggaaatcatctttaccagatcttcaaaaag	571
198			
199			
200	Qy	CCTGGGCCCTGGCAGTCTAGCAGCTTCTCCTGAAATTAATCTTATGAGACTTGAAGAGT	709
201			
202			
203	Db	aaggctcttattacacctgcagctctctcttatttccatcacagt--cagtatcaattctggaag	630
204			
205			
206	Qy	TGTTTGAAGAGACTCTTTTGACGTGCTCTTTACCCAGAGGATACAGTATATAG-CTGGAGG	768
207			
208			
209	Db	aatttccagacattaaagatagtcattcttgggctggtcgtccgctgctgtgtcatggctc	690
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211			
212	Qy	CATTTCCACACTCTGAAATGACCATCTCTGTCTGGTCTTCCTCTGCTGTGTTATGGCC	828
213			
214			
215	Db	atctgctactcgggaatctctaaaaactctgcttcggtgtcgaaatgagaagaagagcac	750
216			
217			
218	Qy	ATCTGTCTACAGGAATCATCAAAACGCTGCTGAGGTGCCCCAGTAAAAA-AA-AGT-AC	885
219			
220			
221	Db	agggctgtgaggcttatcttccaccatcatgattgtttattttctctcttgggtccctac	810
222			
223			
224	Qy	AAGGCCATCGGGCTCAATTTTGTTCATCATGCGGGTGTTTTTCATTTCTCGACACCCCTAC	945
225			
226			
227	Db	aacaattgctcttctctgaaacaccttccagaagaattcttggcctggaataattgcagtagc	870
228			
229			
230	Qy	AATGTGCTATCCTTCTCTCTCTATCAATCCATCTCTATTTGGAAATGACTGTGACGG	1005

RESULT 3
 LOCUS AA671573 447 bp mRNA EST 25-NOV-1997
 DEFINITION v104g01.r2 Soares mouse mammary gland NDMMG Mus musculus cDNA clone
 963216 5' similar to TR:G1322040 G1322040 C-C CHEMOKINE RECEPTOR.
 ; mRNA sequence.
 ACCESSION AA671573
 NID 92643652
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
 Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 447)
 Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
 Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
 Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 Waterston,R.
 TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT

Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of MedicineP
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LNL: contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 MGI:552008

Seq primer: -28ml3 rev2 ET from Amersham
 High quality sequence stop: 397.

FEATURES

Location/Qualifiers
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 /organism="Mus musculus"
 /strain="C57BL/6J"
 /note="Organ: mammary gland; Vector: pT73D-Pac
 (Pharmacia) with a modified polylinker; Site.1: Not I;
 Site.2: Eco RI; 1st strand cDNA was primed with a Not I -
 oligo(dT) primer [5',
 TGTTACCAATCTGAGTGGGAGCGGCCCGAATGCTTTTCTTTTCTTTTCTTTT
 T 3']; double-stranded cDNA was ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of the modified pT73 vector.
 RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
 constructed and normalized by Bento Soares and M. Fatima
 Bonaldo."
 /db_xref="taxon:10090"
 /clone="963216"
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 /sex="male"
 /tissue.type="mammary gland"
 /dev_stage="4 weeks"
 /lab_host="DH10B"
 BASE COUNT 104 a 102 c 92 g 149 t

ORIGIN

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 Best Local Similarity 66.0%; Pred. No. 1.32e-203;
 Matches 293; Conservative 0; Mismatches 146; Indels 5; Gaps 5;
 Db 5 TCACAGGCGCTATACATTTGTTATTTGGTGGAACTCTTCATATCTCTCCCTGACAA 64
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 QY 417 TCTCAGGTTTATACACAGCGCTGTACAGGAGATCTTTTCATATCTCTGCTGACAA 476
 || ||||| ||||| || | | | | ||||| ||||| ||||| ||||| ||||| |||||
 Db 65 TTGATAGGTACTTGCTATTTCCATGCTGTGTTTCTTTAAAGTCAGAACGGTCAACT 124
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 477 TCGACAGGTACCTGGCCATTTGCTATGCTGTGTTTCCCTTCGAGCCGCGACTGTCACT 536
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 Db 125 TTGGGGTGATACAACTGTAGTCATTTGGCGGTGGCTGTGTTTGGCTCTCTCCCGA 184

QY 537 TTGGTGTATCACCAGCATCGTCACCTGGCGCTGGCAGTCTAGCAGCTCTTCTCGAAT 596
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 185 TAATCTTTACCAGATCTCAGAAAGAGGTTTTCATATATACATGCAGTCTCTCATTTTCAC 244
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 597 TTATCTTCTATGAGACTGAAGAGTGTGTTGAAGAGACTCTTTGACAGTCTCTCTTACCAG 656
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 245 ACACCT-CAGTATCATCTCTGGAAGAGTTTCCAAACATTTAAAGATGGTCTATCTTGAGCCTG 303
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 QY 657 AGGATACAGTAT-ATAGCTGGAGGCATTTCCACACTCTGAGAATGACCATCTTCTGTCTC 715
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 Db 304 ATCCCTGCCTCTACTGTCTCATCTGCTACTCAGGAATTTCTCCACACCTCTGTTTCGC 363
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 QY 716 GTTCTCCCTCTGCTGTTATGCCATCTGTACACAGAAATCATCAAAACGCTGCTGAGG 775
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 Db 364 TGTAGGAATGAGAAGAGGACAGGCTGTGAGGCTCATCTTTGCCATCATGATGTC 423
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 QY 776 TGCCCCAGTAAAAA-AA-AGT-ACAAGGCCATCCGGCTCATTTTGTCTATCATGCGCGTG 832
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 Db 424 TACTTTCTCTTCTGGACTCCCTAC 447
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 QY 833 TTTTTCATTTTCTGGACACCCCTAC 856

RESULT 4
 LOCUS AA754459 252 bp mRNA EST 20-JAN-1998
 DEFINITION 97SN1787 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa
 cDNA clone 97SN1787, mRNA sequence.
 ACCESSION AA754459
 NID 92801165
 KEYWORDS EST.
 SOURCE rice.
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Charophyta/Embryophyta group;
 Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
 Poales; Poaceae; Oryza.
 1 (bases 1 to 252)
 Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R., Moon,E.P.,
 Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,
 Lee,M.C. and Eun,M.Y.
 Large-scale sequencing Analysis of ESTs from Rice Immature Seed
 Unpublished (1998)
 TITLE
 JOURNAL
 COMMENT

Contact: Eun M.Y.
 Department of Cytogenetics
 National Inst. of Agri. Sci. and Tech, RDA
 Suwon, Kyunggido, Korea
 Tel: 82 331 290 0301
 Fax: 82 331 290 0307
 Email: myeunesun20.astl.re.kr
 Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
 University, Yongin, Korea. 449-728 bhnahebio@server.myongji.ac.kr
 Seq primer: M13 Reverse Primer.

FEATURES

Location/Qualifiers
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 /organism="Oryza sativa"
 /cultivar="Milyang23"
 /note="Vector: pBluescript SK(+); Site.1: EcoRI; Site.2:
 XhoI; Directional cDNA library inserted into lambda ZAPII
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 /db_xref="taxon:4530"
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 /dev_stage="5 days after pollination"
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BASE COUNT 5 a 21 c 12 g 35 t 179 others
 ORIGIN

Query Match 5.8%; Score 69; DB 12; Length 252;
 Best Local Similarity 13.8%; Pred. No. 1.55e-93;
 Matches 33; Conservative 125; Mismatches 76; Indels 5; Gaps 5;


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Db 15 CBAMTTSYBCHGNBWWVYVASHGNYMSVHNCTBRGTHCDCKKNVNSWTWGTWNBVNS 74
Qy 377 CGGACCTGCTCTTCTGCTCACCCTTCATCTGATCCATATGTCAGGGGGCAATACT 386
Db 75 GDWYWBVBNTKVDVGNHTRCSRWBRVTRMAHYHDYTNBNNNDYHMHBBMYBTGC 134
Qy 387 GGGTTTGGCCATGGCATGTGTAAGCTCCTCTCAGGGTTTATACACACA-GGCTGTGAC 445
Db 135 MTCNMCWBHYNK-TASGWHSTSNYDVKS-STNTWGTBTSYDKSMHGYWCSBBVKYHT 192
Qy 446 AGCGAGATCTTTTTCATAATCTCTGACATCGACAGTACCTGGCCATGTGTCATGCT 505
Db 193 KVSITRATRSYTCVRKYCVW-WMTKKVY-KKYHVVBBCHEHDSKCKTMMWTKNKHVMTS 249
Qy 506 GTGTTTGCCCTTCGAGCCCGGACTGTCACTTTTGGTGTCATCACCAGCATCGTCACCTG 564

RESULT 5
LOCUS AA754459 252 bp mRNA EST 20-JAN-1998
DEFINITION 97SN1787 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa
ACCESSION AA754459
NID 92801165
KEYWORDS EST.
SOURCE rice.
ORGANISM Oryza sativa
Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
Poales; Poaceae; Oryza.
REFERENCE 1 (bases 1 to 252)
AUTHORS Nahn,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R., Moon,E.P.,
Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,
Lee,M.C. and Eun,M.Y.
TITLE Large-scale Sequencing Analysis of ESTs from Rice Immature Seed
JOURNAL Unpublished (1998)
COMMENT
Contact: Eun M.Y.
Department of Cytogenetics
National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
Email: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahn, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
Location/Qualifiers
FEATURES
source
1. .252
/organism="Oryza sativa"
/cultivar="Milyang23"
/notes="vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Directional cDNA library inserted into lambda ZAPII
vector at 5' end with EcoRI and 3' end with Xho I site."
/db_xref="taxon:4530"
/clone="97SN1787"
/clone_lib="Rice Immature Seed Lambda ZAPII cDNA Library"
/tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
BASE COUNT 5 a 21 c 12 g 35 t 179 others
ORIGIN
Query Match 4.7%; Score 56; DB 12; Length 252;
Best Local Similarity 8.3%; Pred. No. 1.28e-65;
Matches 19; Conservative 122; Mismatches 84; Indels 3; Gaps 3;
Db 23 YBCHGNBWWVYVASHGNYMSVHNCTBRGTHCDCKKNVNSWTWGTWNBVNSGDWYWBV 82
Cp 251 CCACATGCCCAAGAGCCGACAGTGAACACAGGAGTACAGCGGGGGGACCAACTGGG 192
Db 83 BNTKVDVGNHTRCSRWBRVTRMAHYHDYTNBNNNDYHMHBBMYBTTGCMTCT-MWC 141
Cp 191 CCATCAGTCTGCTATCAGCTTTTTCACAGACAGCCCGGACGTCATCATAGTAGTG 132

```

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Db 142 WBHNTKCTASGHTSTNVDKS-STNTWGTBTSYDKSMHGYWCSBBVKYHKVSTTRAT 200
Cp 131 TGGTACCAAGGTCATCACTAGTATGAGGTTCATTCATTCCTCCCTGAAAAATC 72
Db 201 RSYTCVRKYCVWMTKKVKKYHVVBBCHEHDSKCKTMMWTKNKHVMT 248
Cp 71 TCITCTAAGTAAAAAC-CGGACGGTGGGTCTTCTATTGATTTCGAT 25

RESULT 6
LOCUS AA754458 247 bp mRNA EST 20-JAN-1998
DEFINITION 97SN1784 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa
ACCESSION AA754458
NID 92801164
KEYWORDS EST.
SOURCE rice.
ORGANISM Oryza sativa
Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
Poales; Poaceae; Oryza.
REFERENCE 1 (bases 1 to 247)
AUTHORS Nahn,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R., Moon,E.P.,
Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,
Lee,M.C. and Eun,M.Y.
TITLE Large-scale Sequencing Analysis of ESTs from Rice Immature Seed
JOURNAL Unpublished (1998)
COMMENT
Contact: Eun M.Y.
Department of Cytogenetics
National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
Email: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahn, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
Location/Qualifiers
FEATURES
source
1. .247
/organism="Oryza sativa"
/cultivar="Milyang23"
/notes="vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Directional cDNA library inserted into lambda ZAPII
vector at 5' end with EcoRI and 3' end with Xho I site."
/db_xref="taxon:4530"
/clone="97SN1784"
/clone_lib="Rice Immature Seed Lambda ZAPII cDNA Library"
/tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
BASE COUNT 7 a 16 c 21 g 34 t 169 others
ORIGIN
Query Match 4.2%; Score 50; DB 12; Length 247;
Best Local Similarity 12.3%; Pred. No. 3.17e-53;
Matches 28; Conservative 104; Mismatches 94; Indels 1; Gaps 1;
Db 1 HWDCTMNTVVRGCCCBANWKNKHTHMTBWCVRVRVTGTTNNGKNGRTTWNDCSDNA 60
Qy 876 CTTCTCATCAATCCATCTTATTGGAATGACTGTGAGCGGAGCAAGCATCTGGACCTGG 935
Db 61 HCRVTBWWYARSKYGYGTBYISWNVDTNTGGTGVGKTTVNVHSGWNNRCSNSVYVWBT 120
Qy 936 TCATGCTGGTGACAGAGGTGATCGCTACTCCACTGCTGCATGACCCCGGTGATCTAGC 995
Db 121 AYCDYBHYBDR-ANHVDTRCTNDRGYCNVTSADNGTSATKRVYTGVDKTDSCGGGCRK 179
Qy 996 CCTTTGTTGGAGAGAGGTTCGGAAGTACCTGCGCCACTTCTCCACAGCACTTGCTCA 1055
Db 180 VTYGSSBYBCGVNVVYVTRTSMKTDSTKMBSDMSRSHVHYGRWM 226

```


For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi/hgi.html>)

For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi/hgi.html>)

For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi/hgi.html>)

Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
Murinae; Mus.
1 (bases 1 to 602)
REFERENCE
AUTHORS
Marra M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Giesel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Septoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, F., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
TITLE
JOURNAL
COMMENT
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MG1:505725
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 388.
FEATURES
Location/Qualifiers
1..602
/organism="Mus musculus"
/strain="C57BL/6J"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCGAAGTTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT73 vector. RNA
provided by Dr. Minoru KO, Wayne State Univ. Library
constructed and normalized by Bento Soares and M.Fatima
Bonaldo."
/db_xref="taxon:10090"
/clone="861637"
/clone_lib="Soares mouse NbMH"
/sex="male"
/tissue_type="heart"
/dev_stage="4 weeks"
/lab_host="DH10B"
BASE COUNT 142 a 164 c 144 g 152 t
ORIGIN
Query Match 2.8%; Score 33; DB 7; Length 602;
Best Local Similarity 64.6%; Pred. No. 8.28e-21;
Matches 73; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
Db 324 CTGTACTCTTCATATTCCTCTCAGTGTCTGGGGAACACGCTGGTATACACGGTCTG 383
QY 209 CTGTACTCTCTGGTGTACATCTGGGCTCTGTGGCAATCTGTGGTGGTATGATCTC 268
Db 384 ATTCGAACAGAGGATCGGACATCTCACCACATCTCTCTCTCTCTCTCTCTCTCT 436
QY 269 ATAAATACAGAGGCTCCGAATTATGACCAACATCTACCTCTCTCTCTCTCTCTCT 321
RESULT 15
LOCUS N70844 310 bp mRNA EST 14-MAR-1996
DEFINITION za73h08.s1 Homo sapiens cDNA clone 298239 3', similar to gb:M1124
HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DQ(4) ALPHA CHAIN
(HUMAN)).
ACCESSION N70844
NID g1227424
KEYWORDS EST.
SOURCE human clone-298239 primer=ml3 -40 forward library=Soares fetal lung
NBHL19W vector=pT73D (Pharmacia) with a modified polylinker
host=DH10B (ampicillin resistant) Rsite1=Not I Rsite2=Eco RI 19
week fetus. 1st strand cDNA was primed with a Not I - oligo(dT)

primer [5'-TGTTACCAATCTGAAGTGGAGCGCGCGCATTTTTTTTTTTTTTTT-3'],
double-stranded cDNA was size selected, ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I and Eco
RI sites of a modified pT73 vector (Pharmacia). Library went
through one round of normalization to a cot = 5. Library
constructed by Bento Soares and M.Fatima Bonaldo.
Homo sapiens
ORGANISM
REFERENCE
AUTHORS
1 (bases 1 to 310)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.
TITLE
JOURNAL
COMMENT
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES
Location/Qualifiers
1..310
/organism="Homo sapiens"
/clone="298239"
BASE COUNT 71 a 73 c 78 g 63 t 25 others
ORIGIN
Query Match 2.7%; Score 32; DB 19; Length 310;
Best Local Similarity 78.7%; Pred. No. 4.40e-19;
Matches 37; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Db 188 CCNCCACATGCCCCAGAGGCCACACGNNAAACCCACAGGNGCAGANC 234
Cp 254 CCACCACATTTGCCAAGAGGCCACACAGTGAACACCA3GGAGTACAGC 208
Search completed: Wed Dec 9 01:11:06 1998
Job time : 3150 secs.

[illegible]

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ch_pp protein - protein database search, using Smith-Waterman algorithm

```

n on: Tue Dec 8 13:11:12 1998; MasPar time 21.71 seconds
      814.247 Million cell updates/sec

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bular output not generated.

tle:
>US-08-963-656-2

Description: (1-355) from US08963656.ppt

Perfect score: 2765

sequence: 1 MTTS LDTVETFGTTSYDDV.....LERTSSVSPSTAEP ELSIVF 355

scoring table: PAM 150
Gap 11

arched: 165420 seqs, 49795644 residues

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st-processing: Minimum Match 0%
Listing first 45 summaries

```

```

database:
  sprembl6
    1:sp_archaea 2:sp_bacteria 3:sp_fungi 4:sp_human
    5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
    9:sp_phase 10:sp_plant 11:sp_rodent 12:sp_unclassified
    13:sp_vertebrate 14:sp_virus

```

statistics: Mean 49.326; Variance 131.433; scale 0.375

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query		Length	DB	ID	Description	Pred. No.
	Score	Match					
1	1921	69.5	359	11	055169	RECEPTOR PROTEIN CKR3.	9.70e-274
2	1914	69.2	359	11	054814	CHEMOKINE RECEPTOR CCR	1.28e-272
3	1513	54.7	352	6	018770	CCR5 RECEPTOR (FRAGMEN	4.71e-209
4	1507	54.5	352	6	062745	CHEMOKINE RECEPTOR CCR	4.17e-208
5	1502	54.3	352	6	062744	CHEMOKINE RECEPTOR CCR	2.57e-207
6	1498	54.2	352	6	062746	CHEMOKINE RECEPTOR CCR	1.10e-206
7	1499	54.2	373	11	055193	CHEMOKINE RECEPTOR CCR	7.66e-207
8	1494	54.0	352	4	015538	CCR5 RECEPTOR (FRAGMEN	4.72e-206
9	1492	54.0	352	6	018771	CCR5 RECEPTOR (FRAGMEN	9.76e-206
10	1489	53.9	352	6	018772	CCR5 RECEPTOR (FRAGMEN	2.91e-205
11	1483	53.6	352	6	062743	CHEMOKINE RECEPTOR CCR	2.57e-204
12	1452	52.5	383	14	089609	G PROTEIN-COUPLED RECE	2.01e-199
13	1442	52.2	360	6	018793	CHEMOKINE RECEPTOR.	7.59e-198
14	1375	49.7	333	4	014694	CCR5 RECEPTOR (FRAGMEN	2.75e-187
15	932	33.7	344	4	000421	CCR6.	4.92e-118
16	877	31.7	384	4	000537	CHEMOKINE RECEPTOR CCR	1.57e-109
17	875	31.6	384	4	000590	CC-CHEMOKINE RECEPTOR	3.19e-109
18	837	30.3	367	11	054869	G PROTEIN-COUPLED RECE	2.30e-103
19	833	30.1	368	13	042444	INTERLEUKIN-8-LIKE RECP	9.49e-103
20	815	29.5	378	11	008707	CHEMOKINE (C-C) RECEPT	5.56e-100

QY 303 FVGERFRKYLRRHFFRHLMLHLGRVIFPLPSEKLERTSVSPSTAEPESLIVF 355

RESULT 2

ID 054814 PRELIMINARY; PRT; 359 AA.

AC 054814;

DT 01-JUN-1998 (TREMBLREL. 06, CREATED)

DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)

DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)

DE CHEMOKINE RECEPTOR CCR3.

OS RATTUS NORVEGICUS (RAT).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; RODENTIA.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=WISTAR; TISSUE=SPLEEN;

RA JIANG Y., SALAFRANCA M.N., ADHIKARI S., XIA Y., FENG L., SONNTAG M.K.,

RA DEFEBRE C.M., PENNELL N.A., STREIT W.J., HARRISON J.K.;

RL J. NEUROIMMUNOL. 0:0-0(1998).

DR EMBL; AF003984; G2897073; -.

SO SEQUENCE 359 AA; 41643 MW; C1FC70CA CRC32;

Query Match 69.2%; Score 1914; DB 11; Length 359;

Best Local Similarity 68.3%; Pred. No. 1, 26e-272;

Matches 241; Conservative 56; Mismatches 53; Indels 3; Gaps 3;

Db 8 LKTVETETTPYEWAPP-CEKVSIRELSWLLPPLYSLVFIVGLGNMVMVYLILIKY 66

QY 5 LDTV-ETGTTSY-YDDVGLCEKADRALMAQFVPLYSLVFTFGLGNVVMVILIKY 62

Db 67 RKLOIMNIYLLNLAISDLLFLFVFPWHVNLWNEWFGHCCKMGLSGLYLYLSEIF 126

QY 63 RLRLIMNIYLLNLAISDLLFLFVFPWHVNLWNEWFGHCCKMGLSGLYLYLSEIF 122

Db 127 FIILLTDYLAIVHVALRALRVTFATITSITWGFVLAALPEFTFHSODNFGDLS 186

QY 123 FIILLTDYLAIVHVALRALRVTFATITSITWGFVLAALPEFTFHSODNFGDLS 182

Db 187 CSPIRYPEGEEDSWKFRHNRNIFGLAPLLIMVICYSGIILTLRCNPKKKRAIOLIF 246

QY 183 CSALYPEDTVSWRHFRLRTIFCLVPLVMAICYTGIIKTLRCPSKKYKAIRLIF 242

Db 247 VVMVIFEFWTPYNNVLLLSAFHSFTELETSQOOSHLDLAQVTEVITHCCINPIYA 306

QY 243 VIMAVFFIWPYNNVLLLSAFHSFTELETSQOOSHLDLAQVTEVITHCCINPIYA 302

Db 307 FVGERFRKHLRFFHRNVAIVRLKRYISPLPGEKLERTSVSPSTAEPESLIVF 359

QY 303 FVGERFRKYLRRHFFRHLMLHLGRVIFPLPSEKLERTSVSPSTAEPESLIVF 355

RESULT 3

ID 018770 PRELIMINARY; PRT; 352 AA.

AC 018770;

DT 01-JAN-1998 (TREMBLREL. 05, CREATED)

DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)

DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)

DE CCR5 RECEPTOR (FRAGMENT).

GN CCR5.

OS PAN TROGLODYTES (CHIMPANZEE).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; PRIMATES.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=MACCRS-140A;

RA ZHANG L., CARRUTHERS C.D., HE T., HUANG Y., CAO Y., WANG G., HAHN B.,

RA HO D.D.;

RL AIDS RES. HUM. RETROVIRUSES 0:0-0(1997).

DR EMBL; AF011538; G2305194; -.

DR PFAM; PF00001; 7tm1.

FT NON_TER 352

SO SEQUENCE 352 AA; 40523 MW; FIC10E99 CRC32;

Query Match 54.7%; Score 1513; DB 6; Length 352;

Best Local Similarity 55.5%; Pred. No. 4, 71e-209;

Matches 186; Conservative 83; Mismatches 57; Indels 9; Gaps 9;

Db 20 COKINKQIAARLLPPLYSLVFIFGFVGNILVLIINCKRLKSMTDIYLLNLAISDLLF 79

QY 24 CEKADTRALMAQFVPLYSLVFTFGLGNVVMVILIKYRLRIMNIYLLNLAISDLLF 83

Db 80 LLVVPWAHAAAQ-WDFGNTMCOLLTGLYFICGFFSIFFIILLTDYLAIVHVAFLK 138

QY 84 LVTLPEWIHVGRHNWVFGHGMCKLLSGFYHTGLYSEIFFIILLTDYLAIVHVAFLR 143

Db 139 ARTVTFGVTSVITWVAVFASLPGLIFTRSQREGLYHT-CSPHFPYSQ-YQFWKNFQTL 196

QY 144 ARTVTFGVTSVITWVAVFASLPGLIFTRSQREGLYHT-ELFEETLCSALYPEDTVYS-WRHFTL 201

Db 197 KIVILGLVPLLVWVICYSGILKTLRCNKKRHRVRLIFTIMIVYFLFWAPYNNVLL 256

QY 202 RMTIFCLVPLVMAICYTGIIKTLRCPS-KKKYKAIRLIFVIMAVFFIWPYNNVAIL 260

Db 257 LNTFQEF-FGLNNCSSNRDLQAMQVETGLMTHCCINPIIYAFVGEKFRNYLLVFFQKH 315

QY 261 LSSVQSILFG-NDCERTKHLDLVMLTEVIAYSHCCMNPVIYAFVGERFRKYLRRHFFHR 319

Db 316 IAKRFCKCCSIFQOEASERASSVYTRSTGQEISV 350

QY 320 LLMHLGRYIPFLPSEKLERTSV-SPSTAEPESLSI 353

RESULT 4

ID 062745 PRELIMINARY; PRT; 352 AA.

AC 062745;

DT 01-AUG-1998 (TREMBLREL. 07, CREATED)

DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)

DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)

DE CHEMOKINE RECEPTOR CCR5.

OS CERCOBUS TORQUATUS ATYS (RED-CROWNED MANGABEY) (SOOTY MANGABEY).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; PRIMATES.

RN [1]

RP SEQUENCE FROM N.A.

RA CHEN Z., GETTIE A., HO D.D., MARX P.A.;

RL VIROLOGY 0:0-0(1998).

DR EMBL; AF051904; G3135300; -.

SO SEQUENCE 352 AA; 40460 MW; E6A5AA07 CRC32;

Query Match 54.5%; Score 1507; DB 6; Length 352;

Best Local Similarity 55.2%; Pred. No. 4, 17e-208;

Matches 185; Conservative 85; Mismatches 56; Indels 9; Gaps 9;

Db 20 COKINKQIAARLLPPLYSLVFIFGFVGNILVLIINCKRLKSMTDIYLLNLAISDLLF 79

QY 24 CEKADTRALMAQFVPLYSLVFTFGLGNVVMVILIKYRLRIMNIYLLNLAISDLLF 83

Db 80 LLVVPWAHAAAQ-WDFGNTMCOLLTGLYFICGFFSIFFIILLTDYLAIVHVAFLK 138

QY 84 LVTLPEWIHVGRHNWVFGHGMCKLLSGFYHTGLYSEIFFIILLTDYLAIVHVAFLR 143

Db 139 ARTVTFGVTSVITWVAVFASLPGLIFTRSQREGLYHT-CSPHFPYSQ-YQFWKNFQTL 196

QY 144 ARTVTFGVTSVITWVAVFASLPGLIFTRSQREGLYHT-ELFEETLCSALYPEDTVYS-WRHFTL 201

Db 197 KIVILGLVPLLVWVICYSGILKTLRCNKKRHRVRLIFTIMIVYFLFWAPYNNVLL 256

QY 202 RMTIFCLVPLVMAICYTGIIKTLRCPS-KKKYKAIRLIFVIMAVFFIWPYNNVAIL 260

Db 257 LNTFQEF-FGLNNCSSNRDLQAMQVETGLMTHCCINPIIYAFVGEKFRNYLLVFFQKH 315

QY 261 LSSVQSILFG-NDCERTKHLDLVMLTEVIAYSHCCMNPVIYAFVGERFRKYLRRHFFHR 319

Db 316 IAKRFCKCCSIFQOEASERASSVYTRSTGQEISV 350

QY 320 LLMHLGRYIPFLPSEKLERTSV-SPSTAEPESLSI 353


```

DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DE 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DN CCR5 RECEPTOR (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RA ZHANG L., CARRUTHERS C.D., HE T., HUANG Y., CAO Y., WANG G., HAHN B.,
RA HO D.D.;
RL AIDS RES. HUM. RETROVIRUSES 0:0-0(1997).
DR ENBL; AF011536; G2305190; -.
DR ENBL; AF011536; G2305190; -.
DR ENBL; AF011534; G2305186; -.
DR PFAM; PF00001; 7tm.1.
FT NON_TER 352
SO SEQUENCE 352 AA; 40552 MW; BLECA8D9 CRC32;

Query Match 54.0%; Score 1494; DB 4; Length 352;
Best Local Similarity 54.3%; Pred. No. 4.72e-206;
Matches 182; Conservative 87; Mismatches 57; Indels 9; Gaps 9;

20 COKINVKQIAARLLPPLYSLVFIQFVGNMVLVILILNCKRLKSMTDIYLLNLAISDLFF 79
24 CEKADTRALMAQFVPPPLYSLVFTGLGNVVMILIKYRRLRMTNIYLLNLAISDLFF 83
80 LLTPVFWAHYAAQ-WDFGNTMQLLTGLYFIFGFSGIFFIILLTIDRYLAIVHAVFALK 138
84 LVTLPFWIHYVRGNWVFGHGMCKLLSGFYHTGLYSEIFFIILLTIDRYLAIVHAVFALK 143
139 ARTVFGVTSVITVWVAVFASLPGIIFTRSQKGLHYT-CSSHFPYSQ-YQFKNFQTL 196
144 ARTVFGVITSVITWGLAVLAALPEFIFYETE-ELFEETLCSALYPEDTVYS-WRHFHTL 201
197 KIVILGLVPLVMVICYSGILKTLRCRNEKRRHRAVRLFTIMIVYFLFWAPYDIVLL 256
202 RMTIFCLVPLVMAICYTGIIKTLRCPG-KKKYKAILRIFVIMAVFFIFTWPNVAIL 260
257 LNTFQEF-FGLNCCSSNRLDQAMQVETGLMTHCCINPIIYAFVGEKFRNLLVFFQKH 315
261 LSSYSQILFG-NDCERTKHLDMVLVTEVIAYSHCCMNPVIYAFVGERFKYLRHFFHRH 319
320 LLMHLGRYIPFLPSEKLERTSSV-SPSTAEPELSI 353

RESULT 9
OI8771; PRELIMINARY; PRT; 352 AA.
01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
CCR5 RECEPTOR (FRAGMENT).
OS PAN TROGLODYTES (CHIMPANZEE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RA ZHANG L., CARRUTHERS C.D., HE T., HUANG Y., CAO Y., WANG G., HAHN B.,
RA HO D.D.;
RL AIDS RES. HUM. RETROVIRUSES 0:0-0(1997).
DR ENBL; AF011541; G2305200; -.
DR PFAM; PF00001; 7tm.1.
FT NON_TER 352
SO SEQUENCE 352 AA; 40598 MW; A9BF8EDF CRC32;

Query Match 53.9%; Score 1489; DB 6; Length 352;
Best Local Similarity 54.0%; Pred. No. 2.91e-205;
Matches 181; Conservative 88; Mismatches 57; Indels 9; Gaps 9;

20 COKINVKQIAARLLPPLYSLVFIQFVGNMVLVILILNCKRLKSMTDIYLLNLAISDLFF 79
24 CEKADTRALMAQFVPPPLYSLVFTGLGNVVMILIKYRRLRMTNIYLLNLAISDLFF 83
80 LLTPVFWAHYAAQ-WDFGNTMQLLTGLYFIFGFSGIFFIILLTIDRYLAIVHAVFALK 138
84 LVTLPFWIHYVRGNWVFGHGMCKLLSGFYHTGLYSEIFFIILLTIDRYLAIVHAVFALK 143
139 ARTVFGVTSVITVWVAVFASLPGIIFTRSQKGLHYT-CSSHFPYSQ-YQFKNFQTL 196
144 ARTVFGVITSVITWGLAVLAALPEFIFYETE-ELFEETLCSALYPEDTVYS-WRHFHTL 201
197 KIVILGLVPLVMVICYSGILKTLRCRNEKRRHRAVRLFTIMIVYFLFWAPYDIVLL 256
202 RMTIFCLVPLVMAICYTGIIKTLRCPG-KKKYKAILRIFVIMAVFFIFTWPNVAIL 260
257 LNTFQEF-FGLNCCSSNRLDQAMQVETGLMTHCCINPIIYAFVGEKFRNLLVFFQKH 315
261 LSSYSQILFG-NDCERTKHLDMVLVTEVIAYSHCCMNPVIYAFVGERFKYLRHFFHRH 319
316 IAKRFCKCSIFQOEAPERASSVYTRSTGQEISV 350

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Db 20 COKINVKQIAARLLPPLYSLVFIQFVGNMVLVILILNCKRLKSMTDIYLLNLAISDLFF 79
QY 24 CEKADTRALMAQFVPPPLYSLVFTGLGNVVMILIKYRRLRMTNIYLLNLAISDLFF 83
Db 80 LLTPVFWAHYAAQ-WDFGNTMQLLTGLYFIFGFSGIFFIILLTIDRYLAIVHAVFALK 138
QY 84 LVTLPFWIHYVRGNWVFGHGMCKLLSGFYHTGLYSEIFFIILLTIDRYLAIVHAVFALK 143
Db 139 ARTVFGVTSVITVWVAVFASLPGIIFTRSQKGLHYT-CSSHFPYSQ-YQFKNFQTL 197
QY 144 ARTVFGVITSVITWGLAVLAALPEFIFYETEELFEETLCSALYPEDTVYS-WRHFHTL 202
Db 198 IIVILGLVPLVMVICYSGILKTLRCRNEKRRHRAVRLFTIMIVYFLFWAPYDIVLL 257
QY 203 MTFICLVPLVMAICYTGIIKTLRCPG-KKKYKAILRIFVIMAVFFIFTWPNVAIL 261
Db 258 NTFQEF-FGLNCCSSNRLDQAMQVETGLMTHCCINPIIYAFVGEKFRNLLVFFQKH 316
QY 262 SSSYSQILFG-NDCERTKHLDMVLVTEVIAYSHCCMNPVIYAFVGERFKYLRHFFHRH 320
Db 317 AKRFCKCSIFQOEAPERASSVYTRSTGQEISV 350
QY 321 LLMHLGRYIPFLPSEKLERTSSV-SPSTAEPELSI 353

RESULT 10
OI8772; PRELIMINARY; PRT; 352 AA.
01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
CCR5 RECEPTOR (FRAGMENT).
OS PAN TROGLODYTES (CHIMPANZEE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RA ZHANG L., CARRUTHERS C.D., HE T., HUANG Y., CAO Y., WANG G., HAHN B.,
RA HO D.D.;
RL AIDS RES. HUM. RETROVIRUSES 0:0-0(1997).
DR ENBL; AF011541; G2305200; -.
DR PFAM; PF00001; 7tm.1.
FT NON_TER 352
SO SEQUENCE 352 AA; 40598 MW; A9BF8EDF CRC32;

Query Match 53.9%; Score 1489; DB 6; Length 352;
Best Local Similarity 54.0%; Pred. No. 2.91e-205;
Matches 181; Conservative 88; Mismatches 57; Indels 9; Gaps 9;

20 COKINVKQIAARLLPPLYSLVFIQFVGNMVLVILILNCKRLKSMTDIYLLNLAISDLFF 79
QY 24 CEKADTRALMAQFVPPPLYSLVFTGLGNVVMILIKYRRLRMTNIYLLNLAISDLFF 83
Db 80 LLTPVFWAHYAAQ-WDFGNTMQLLTGLYFIFGFSGIFFIILLTIDRYLAIVHAVFALK 138
QY 84 LVTLPFWIHYVRGNWVFGHGMCKLLSGFYHTGLYSEIFFIILLTIDRYLAIVHAVFALK 143
Db 139 ARTVFGVTSVITVWVAVFASLPGIIFTRSQKGLHYT-CSSHFPYSQ-YQFKNFQTL 196
QY 144 ARTVFGVITSVITWGLAVLAALPEFIFYETE-ELFEETLCSALYPEDTVYS-WRHFHTL 201
Db 197 KIVILGLVPLVMVICYSGILKTLRCRNEKRRHRAVRLFTIMIVYFLFWAPYDIVLL 256
QY 202 RMTIFCLVPLVMAICYTGIIKTLRCPG-KKKYKAILRIFVIMAVFFIFTWPNVAIL 260
Db 257 LNTFQEF-FGLNCCSSNRLDQAMQVETGLMTHCCINPIIYAFVGEKFRNLLVFFQKH 315
QY 261 LSSYSQILFG-NDCERTKHLDMVLVTEVIAYSHCCMNPVIYAFVGERFKYLRHFFHRH 319
316 IAKRFCKCSIFQOEAPERASSVYTRSTGQEISV 350

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RA CHEN C.N., EVANS C., FITZGERALD M., SEE L.H., TANG M
RA GNOJ L., LA BASTIDE M., KAPLAN N., GRECO T., TOUCHMAN

Search completed: Tue Dec 8 13:12:41 1998
Job time : 89 secs.

DR EMBL: AF026535: G2582566; -
 DR GCRDB: GCR_0988; -
 DR GCRDB: GCR_1931; -
 DR GCRDB: GCR_1934; -
 DR GCRDB: GCR_1993; -
 DR GCRDB: GCR_1993; -
 DR GCRDB: GCR_2529; -
 DR MIM: 601268; -
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; 1.
 KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE.
 FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 35 62 1 (POTENTIAL).
 FT DOMAIN 63 72 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 73 93 2 (POTENTIAL).
 FT DOMAIN 94 107 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 108 129 3 (POTENTIAL).
 FT DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 147 171 4 (POTENTIAL).
 FT DOMAIN 172 203 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 204 223 5 (POTENTIAL).
 FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 240 264 6 (POTENTIAL).
 FT DOMAIN 265 281 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 282 305 7 (POTENTIAL).
 FT DOMAIN 306 355 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 106 183 BY SIMILARITY.
 FT CONFLICT 276 S -> T (IN REF. 4).
 SQ SEQUENCE 355 AA; 41043 MW; EB145247 CRC32;

Query Match 99.4%; Score 2748; DB 1; Length 355;
 Best Local Similarity 99.4%; Pred. No. 0.00e+00;
 Matches 353; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 MTSLDVTETGTTSYDDVGLLCEKADTRALMAQVPPVLSLVFTVGLGNVVMILI 60
 Qy 1 MTSLDVTETGTTSYDDVGLLCEKADTRALMAQVPPVLSLVFTVGLGNVVMILI 60

Db 61 KYRRLRIMNTIYLLNLAISDLLFLTPFWHYHVRGNWVFGHGCKLLSGFYHTGLYSE 120
 Qy 61 KYRRLRIMNTIYLLNLAISDLLFLTPFWHYHVRGNWVFGHGCKLLSGFYHTGLYSE 120

Db 121 IFFIILLTIDRYLAIVHAVFALRARTVTFGVTISVTWGLAVLALPFIYETEELFEE 180
 Qy 121 IFFIILLTIDRYLAIVHAVFALRARTVTFGVTISVTWGLAVLALPFIYETEELFEE 180

Db 181 TLCSALYPEDTVYSWRHFHTLRMTIFCLVPLLVMAICYTGIIKTLRCPKSKKYKAIRL 240
 Qy 181 TLCSALYPEDTVYSWRHFHTLRMTIFCLVPLLVMAICYTGIIKTLRCPKSKKYKAIRL 240

Db 241 IFVINAVFFIFTWPNVAILSSYSILFGNDCERSKHLDLVLMVTEVIAYSHCCMNPI 300
 Qy 241 IFVINAVFFIFTWPNVAILSSYSILFGNDCERSKHLDLVLMVTEVIAYSHCCMNPI 300

Db 301 YAFVGERFKYLRHFFHRLHMLGRYIPFLPSEKLETSVSPSTAPPELSIVF 355
 Qy 301 YAFVGERFKYLRHFFHRLHMLGRYIPFLPSEKLETSVSPSTAPPELSIVF 355

RESULT 2
 ID CKR3_CERAE STANDARD; PRT; 355 AA.
 AC P56492;
 DT 15-JUL-1998 (REL. 36, CREATED)
 DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE C-C CHEMOKINE RECEPTOR TYPE 3 (C-C CKR-3) (CCR-3).
 GN CMKBR3.
 OS CERCOPITHECUS AETHIOPS (GREEN MONKEY) (GRIVET).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA SOL N., TREBOUTE C., GOMAS E., FERCHAL F., ALIZON M.;
 RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DOBJ DATA BANKS.
 CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO EOTAXIN,

CC MCP-3, MCP-4 AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
 CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL: Y13775; E1191907; -
 DR GCRDB: GCR_2422; -
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; 1.
 KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE.
 FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 35 62 1 (POTENTIAL).
 FT DOMAIN 63 72 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 73 93 2 (POTENTIAL).
 FT DOMAIN 94 107 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 108 129 3 (POTENTIAL).
 FT DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 147 171 4 (POTENTIAL).
 FT DOMAIN 172 203 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 204 223 5 (POTENTIAL).
 FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 240 264 6 (POTENTIAL).
 FT DOMAIN 265 281 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 282 305 7 (POTENTIAL).
 FT DOMAIN 306 355 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 106 183 BY SIMILARITY.
 SQ SEQUENCE 355 AA; 40830 MW; AED65DF8 CRC32;

Query Match 91.8%; Score 2539; DB 1; Length 355;
 Best Local Similarity 91.5%; Pred. No. 0.00e+00;
 Matches 325; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

Db 1 MTSLYVTEFGPTSYDDMGLLCEKADVGALIAQVPPVLSLVFTVGLGNVVMILI 60
 Qy 1 MTSLDVTETGTTSYDDVGLLCEKADTRALMAQVPPVLSLVFTVGLGNVVMILI 60

Db 61 KYRRLRIMNTIYLLNLAISDLLFLTPFWHYHVRGNWVFGHGCKLVSLGYHTGLYSE 120
 Qy 61 KYRRLRIMNTIYLLNLAISDLLFLTPFWHYHVRGNWVFGHGCKLVSLGYHTGLYSE 120

Db 121 IFFIILLTIDRYLAIVHAVFALRARTVTFGVTISVTWGLAVLALPFIYETEELFEE 180
 Qy 121 IFFIILLTIDRYLAIVHAVFALRARTVTFGVTISVTWGLAVLALPFIYETEELFEE 180

Db 181 TLCSALYPEDTVYSWRHFHTLRMTIFCLVPLLVMAICYTGIIKTLRCPKSKKYKAIRL 240
 Qy 181 TLCSALYPEDTVYSWRHFHTLRMTIFCLVPLLVMAICYTGIIKTLRCPKSKKYKAIRL 240

Db 241 IFVINAVFFIFTWPNVAILSSYSILFGNDCERSKHLDLVLMVTEVIAYSHCCMNPI 300
 Qy 241 IFVINAVFFIFTWPNVAILSSYSILFGNDCERTKHLDLVLMVTEVIAYSHCCMNPI 300

Db 301 YAFVGERFKYLRHFFHRLHMLGRYIPFLPSEKLETSVSPSTAPPELSIVF 355
 Qy 301 YAFVGERFKYLRHFFHRLHMLGRYIPFLPSEKLETSVSPSTAPPELSIVF 355

RESULT 3
 ID CKR3_MACMU STANDARD; PRT; 355 AA.
 AC P56483;
 DT 15-JUL-1998 (REL. 36, CREATED)
 DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE C-C CHEMOKINE RECEPTOR TYPE 3 (C-C CKR-3) (CCR-3).
 GN CMKBR3.
 OS MACACA MULATTA (RHESUS MACAQUE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA HAUER D.A., MARGULIES B.J., CLEMENTS J.E.;
 RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DOBJ DATA BANKS.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA SOL N., TREBOUTE C., GOMAS E., FERCHAL F., ALIZON M.;

RP SEQUENCE FROM N.A.
RC SPECIES=M.MULATTA;
RA HAUSER D.A., MARGULIES B.-J., CLEMENTS J.E.;
RL SUBMITTED (APR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=M.MULATTA, M.FASCICULARIS, AND M.NEMESTRINA;
RX MEDLINE; 97268687.
RA EDINGER A.L., AMEDEE A., MILLER K., DORANZ B.J., ENDRES M.,
RA SHARRON M., SAMSON M., LU Z.H., CLEMENTS J.E., MURPHY-CORB M.,
RA PEPPER S.C., PARMENTIER M., BRODER C.C., DOMS R.W.;
RL PROC. NATL. ACAD. SCI. U.S.A. 94:4005-4010(1997).
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC DIFFERENTIATION.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; U7672; G1850350; -
DR EMBL; U73739; G1771981; -
DR EMBL; U96762; G2088633; -
DR EMBL; AF005660; G2245614; -
DR EMBL; AF005661; G2245616; -
DR EMBL; AF005662; G2245618; -
DR GCRDB; GCR_1296; -
DR GCRDB; GCR_1369; -
DR GCRDB; GCR_1370; -
DR GCRDB; GCR_1371; -
DR GCRDB; GCR_1639; -
DR GCRDB; GCR_1641; -
DR PROSITE; PS00237; G-PROTEIN_RECEPTOR; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.
FT DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT DOMAIN 302 352
FT TRANSMEM 352 352
FT DISULFID 101 178
FT CARBOHYD 268 268
FT CONFLICT 241 241
FT CONFLICT 292 292
SQ SEQUENCE 352 AA; 40507 MW; 9B6826EC CRC32;

Query Match 54.9%; Score 1519; DB 1; Length 352;
Best Local Similarity 55.5%; Pred. No. 1.21e-232;
Matches 186; Conservative 84; Mismatches 56; Indels 9; Gaps 9;

Db 20 COKINVKOIAARLLPPLYSLVFIFGVGNILVLLINCKRLKSKMTDIYLLNLAISDLFF 79
Qy 24 CEKADTRALMAQFVPPYLSLVFTGLGNVVMILLKYRLRINTNYLLNLAISDLFF 83
Db 80 LTVVPFWAHYAAQ-WDFGNMTCOLLGLYFGFSGIFFILLTIDRYLAIVHAFALK 138
Qy 84 LVTLPFWHYVRGHNWVFGHGMCKLLSGFYHTGLYSEIFFILLTIDRYLAIVHAFALR 143
Db 139 ARTVTEGVTVITWVAVFASLPGIITRSQREGLHYT-CSSHFPYSQ-YQFWKNFQTL 196
Qy 144 ARTVTEGVTVITWVAVFASLPGIITRSQREGLHYT-ELFETLCSALYPTDVTYS-WRHFHTL 201
Db 197 KMWILGLVPLVMVVCYSGIKTLRLCRNEKKRRHVRVLIPTIMVYFLFWAPYNI 256
Qy 202 RMTIFCLVPLVMAICVTGIKTLRLCRPS-KKKYKARLIFVMAVEFFIETWYNVAIL 260

Db 257 LNTQEP-FGLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFVGEKFRNVLVFFOKH 315
Qy 261 LSSYSILFG-NDCERTKHLDMVLTVEIAYSHCCNPNVIYAFVGERFRKYLRRHFRH 319
Db 316 IAKRFCKCSIFQOEAPERASSVYTRSTGEOEISV 350
Qy 320 LMLHGRYIPFLPSEKLERTSSV-SPSTAEPPELSI 353

RESULT 9
ID CKR5_CERAE STANDARD; PRT; 352 AA.
AC P56493; 1998 (REL. 36, CREATED)
DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CMKBR5
OS CERCOITHECUS AETHIOPS (GREEN MONKEY) (GRIVET).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=KIDNEY;
RX MEDLINE; 98001387.
RA KUHMAN S.E., PLATT E.J., KOZAK S.L., KABAT D.;
RL J. VIROL. 71:8642-8656(1997).
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC DIFFERENTIATION.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; U83324; G2347108; -
DR EMBL; U83325; G2347110; -
DR GCRDB; GCR_2465; -
DR GCRDB; GCR_2466; -
DR PROSITE; PS00237; G-PROTEIN_RECEPTOR; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; POLYMORPHISM.
FT DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT DOMAIN 302 352
FT DISULFID 101 178
FT VARIANT 14 14
FT VARIANT 352 352
SQ SEQUENCE 352 AA; 40561 MW; 9CA7E235 CRC32;

Query Match 54.6%; Score 1511; DB 1; Length 352;
Best Local Similarity 55.2%; Pred. No. 3.04e-231;
Matches 186; Conservative 84; Mismatches 58; Indels 9; Gaps 9;

Db 20 COKINVKOIAARLLPPLYSLVFIFGVGNILVLLINCKRLKSKMTDIYLLNLAISDLFF 79
Qy 24 CEKADTRALMAQFVPPYLSLVFTGLGNVVMILLKYRLRINTNYLLNLAISDLFF 83
Db 80 LTVVPFWAHYAAQ-WDFGNMTCOLLGLYFGFSGIFFILLTIDRYLAIVHAFALK 138
Qy 84 LVTLPFWHYVRGHNWVFGHGMCKLLSGFYHTGLYSEIFFILLTIDRYLAIVHAFALR 143
Db 139 ARTVTEGVTVITWVAVFASLPGIITRSQREGLHYT-CSSHFPYSQ-YQFWKNFQTL 196


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FT DOMAIN 221 237
FT TRANSMEM 238 262
FT DOMAIN 239 279
FT TRANSMEM 280 303
FT DOMAIN 304 354
FT DISULFID 103 180
FT CARBOHYD 270 270
FT VARIANT 11 11
FT VARIANT 62 62
FT VARIANT 66 66
FT VARIANT 97 97
FT VARIANT 109 109
FT VARIANT 156 156
FT VARIANT 160 160
FT VARIANT 185 185
FT VARIANT 213 213
FT VARIANT 318 318
FT VARIANT 337 337
FT CONFLICT 3 3
FT CONFLICT 80 80
FT CONFLICT 190 190
FT CONFLICT 208 208
FT CONFLICT 145 145
FT CONFLICT 145 145
SEQUENCE 354 AA; 40863 MW; 6ECD306A CRC32;

Query Match 54.2%; Score 1500; DB 1; Length 354;
Best Local Similarity 54.4%; Pred. No. 2,556-229;
Matches 181; Conservative 83; Mismatches 62; Indels 7; Gaps 7;

Db 22 COKINKVQAOLPLLYSLVIFGFGVMVFLILISCKLKSVTDIYLLNLAISDLFL 81
QY 24 CEKADTRALMAQFVPLYSVLVTFGLLGNVVMVILIKYRLRIMNLYLLNLAISDLFL 83
Db 82 LITLPEWHAHA-ANEMIFGNIMKVFYGYHGGIFFIILLTIDRYLAIVHAFVALK 140
QY 84 LVTLPWIVHVRGNVWFGHGMCKLSGYHTGLYSEIFFIILLTIDRYLAIVHAFVLR 143
Db 141 VRTVNEGVITSVTVWVAVFASIPELIIFTRSQEGFHYT-CSPHPHTQYHFWKSFQILK 199
QY 144 ARTVFGVITSVITVGLAVLAALPEEFYFETE-ELFEETLCSALYPDTVYSWRHFHTLR 202
Db 200 MWLSLILPLLVMIICYSGILHTFCRNEKRRHRAVRILFIMIVYFLFWTPYNNVILL 259
QY 203 MIFCLVPLLVMAICYTGIIITLRCPS-KKYYKAIRLIFVIMAVFFIFTWPNVAILL 261
Db 260 TTFQEF-FGLNCCSSNRDLQAMQATETLGMTHCCLNPIVYAFVGEKFSYLSVFFRKHI 318
QY 262 SSVQSILFG-NDCEKTKHLDVLMVLVTEVIAYSHCCMNPVYAFVGERFRKYLHFFHRL 320
Db 319 VRFCKRCSIFQODNPDVSSVYTRSTGHEVS 351
QY 321 LMHLGRYIPFLPSEKLERTSSV-SPSTARPELS 352

RESULT 15
ID CKRS_HUMAN STANDARD; PRT; 352 AA.
AC P51681; O14692; O14693; O14695; O14696; O14697; O14698; O14699;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CKR-5) (CCR-5) (CCR5)
DE (HIV-1 FUSION CO-RECEPTOR) (CHEMR13).
GN CMKRS.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96241590.
RA SAMSON M., LABBE O., MOLLEREAU C., VASSART G., PARMENTIER M.;
RL BIOCHEMISTRY 35:3362-3367(1996).
RN [2]
RP SEQUENCE FROM N.A.
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RX MEDLINE; 96291862.
RA RAPORT C.J., GOSLING J., SCHWEICHAERT V.L., GRAY P.W., CHARO I.F.;
RL J. BIOL. CHEM. 271:17161-17166(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96295970.
RA COMBADIERE C., AHUJA S.K., TIFFANY H.L., MURPHY P.M.;
RL J. LEUKOC. BIOL. 60:147-152(1996).
RN [4]
RP SEQUENCE FROM N.A.
RA MCCOMBIE W.R., WILSON R., CHEN E., GIBBS R., ZUO L., JOHNSON D.,
RA NHAN M., PARNELL L., DEDHIA N., ANSARI A., MARDIS E., SCHUTZ K.,
RA GNOI L., LA BASTIDE M., KAPLAN N., GRECO T., TOUCHMAN J., TANG M.,
RA MUZY D., CHEN C.N., EVANS C., FITZGERALD M., SEE L.H., TANG M.,
RA PORCEL B.M., DRAGAN Y., GIACALONE J., PAE A., POWELL E.,
RA SOLINSKY K.A., DESILVA U., DIAZ-PEREZ S., ZHOU X., YU Y.,
RA WATANABE M., DOGETT N., GARCIA D., SAGRIPANTI J.L.;
RL SUBMITTED (MAY-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE; 98001387.
RA KUHMANN S.E., PLATT E.J., KOZAK S.L., KABAT D.;
RL J. VIROL. 71:8642-8656(1997).
RN [6]
RP SEQUENCE FROM N.A., AND POLYMORPHISMS.
RX MEDLINE; 98022612.
RA ZHANG L., CARRUTHERS C.D., HE T., HUANG Y., CAO Y., WANG G., HAHN B.,
RA HO D.D.;
RL AIDS RES. HUM. RETROVIRUSES 13:1357-1366(1997).
RN [7]
RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
RX MEDLINE; 96260017.
RA DENG H., LIU R., ELMETIER W., CHOE S., UNUTMAZ D., BURKHART M.,
RA DI MARZIO P., MARZON S., SUTTON R.E., HILL C.M., DAVIS C.B.,
RA PEIPER S.C., SCHALL T.J., LITTMAN D.R., LANDAU N.R.;
RL NATURE 381:661-666(1996).
RN [8]
RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
RX MEDLINE; 96260018.
RA DRAGIC T., LITWIN V., ALLAWAY G.P., MARTIN S.R., HUANG Y.,
RA NAGASHIMA K.A., CAVANAN C., MADDON P.J., KOUP R.A., MOORE J.P.,
RA PAXTON W.A.;
RL NATURE 381:667-673(1996).
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC DIFFERENTIATION.
CC -!- FUNCTION: ACTS AS CO-RECEPTOR WITH CD4 FOR PRIMARY NON-
CC SYNCYTUM-INDUCING STRAINS (NSI) (MACROPHAGE-TROPIC) OF HIV-1
CC VIRUS. IT PROMOTES ENV-MEDIATED FUSION OF THE VIRUS.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: FOUND IN PROMYELOCYTIC CELLS.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; X91492; E199247; -
DR EMBL; U54994; G1457946; -
DR EMBL; U57840; G1502409; -
DR EMBL; U95626; G2104520; -
DR EMBL; U83326; G2347112; -
DR EMBL; AF011500; G2305118; -
DR EMBL; AF011501; G2305120; -
DR EMBL; AF011502; G2305122; -
DR EMBL; AF011503; G2305124; -
DR EMBL; AF011505; G2305128; -
DR EMBL; AF011506; G2305130; -
DR EMBL; AF011507; G2305132; -
DR EMBL; AF011508; G2305134; -
DR EMBL; AF011509; G2305136; -
DR EMBL; AF011510; G2305138; -
DR EMBL; AF011511; G2305140; -
DR EMBL; AF011512; G2305142; -
DR EMBL; AF011513; G2305144; -
DR EMBL; AF011514; G2305146; -
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WQSELEH (TM)

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ch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Dec 8 13:19:33 1998; MasPar time 11.52 Seconds
Tabular output not generated. 498.610 Million cell updates/sec

Title: >US-08-963-656-4
Description: (1-355) from US08963656.pep
Perfect Score: 2760
Sequence: 1 MTTSLDVTETGTSYDDV.....LERTSSVSPSTAEPELSIVF 355

Scoring table: PAM 150
Gap 11

Searched: 131922 seqs, 16180660 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29

Statistics: Mean 34.811; Variance 169.172; scale 0.206

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description	Pred. No.
1	2760	100.0	355	28	Human eosinophil eota	2.88e-228
2	2760	100.0	355	24	Human chemokine recep	2.88e-228
3	2760	100.0	355	19	CC-chemokine receptor	2.88e-228
4	2758	99.9	355	23	Human C-C chemokine r	4.32e-228
5	2758	99.9	355	19	CC-chemokine receptor	4.32e-228
6	2722	98.6	355	26	Human CCR3 chemokine	6.57e-225
7	2668	96.7	355	19	CC-chemokine receptor	3.89e-220
8	1834	66.4	355	11	Human MIP-1 alpha/RAN	1.32e-146
9	1834	66.4	355	25	Human MIP-1 alpha/RAN	1.32e-146
10	1834	66.4	355	24	Human MIP-lalpha/RANT	1.32e-146
11	1726	62.5	355	24	Rat CC chemokine rece	4.07e-137
12	1497	54.2	352	24	Macaque chemokine rec	4.95e-117
13	1484	53.8	352	27	Human chemokine recep	6.81e-116
14	1484	53.8	352	27	Human CCR5	6.81e-116
15	1484	53.8	352	29	Human CC chemokine re	6.81e-116
16	1485	53.8	371	29	Human CC chemokine re	5.57e-116
17	1471	53.3	352	20	Human G-protein chemo	9.37e-115
18	1421	51.5	360	14	Human monocyte chemoa	2.23e-110

19	1421	51.5	360	26	W35833	Human monocyte chemoa	2.23e-110
20	1378	49.9	332	28	W26766	Human chemokine recep	1.28e-106
21	1335	48.4	374	14	R79165	Human monocyte chemoa	7.35e-103
22	1238	44.9	360	19	R99274	Chemokine receptor K5	2.16e-94
23	1067	38.7	355	20	W07618	Human G-protein recep	1.66e-79
24	1011	36.6	355	11	R53748	Seven transmembrane r	1.20e-74
25	940	34.1	356	29	W48087	Human macrophage/dend	1.70e-68
26	927	33.6	344	28	W26767	Human chemokine recep	2.27e-67
27	825	29.9	358	11	R53745	Partial sequence of s	1.45e-58
28	825	29.9	410	11	R53743	Putative seven transm	1.45e-58
29	822	29.8	378	11	R53744	Human dendritic cell	2.63e-58
30	794	28.8	365	29	W48086	Human dendritic cell	6.76e-56
31	796	28.8	378	10	R54079	Epstein Barr virus in	4.55e-56
32	790	28.6	184	27	W27406	Inactive human CCR5	1.49e-55
33	790	28.6	215	27	W27408	Inactive human CCR5	1.49e-55
34	765	27.7	359	11	R53747	Seven transmembrane r	2.10e-53
35	739	26.8	355	7	R33420	Human IL-8 receptor f	3.58e-51
36	739	26.8	360	15	R80758	Interleukin 8 recepto	3.58e-51
37	739	26.8	360	6	R28273	Sequence in a low aff	3.58e-51
38	739	26.8	1064	14	R70124	IL8-R type 2-GFP 130	3.58e-51
39	725	26.3	350	15	R80951	Recombinant high affi	5.68e-50
40	725	26.3	350	12	R68811	Interleukin-8 recepto	5.68e-50
41	725	26.3	350	15	R80756	Interleukin 8 recepto	5.68e-50
42	725	26.3	415	23	W19780	Human G-protein chemo	5.68e-50
43	725	26.3	1060	14	R70123	IL8-R type 1-GFP 130	5.68e-50
44	719	26.1	352	12	R68812	Human monocyte PF1AR	1.85e-49
45	721	26.1	360	15	R80953	Recombinant high affi	1.25e-49

ALIGNMENTS

RESULT 1

ID W31850 standard; Protein; 355 AA.

AC W31850;

DT 07-MAY-1998 (first entry)

DE Human eosinophil eotaxin receptor protein CC CCR3.

KW Eosinophil eotaxin receptor; CC CCR3; human; treatment; dermatitis;

KW atopic condition; allergic rhinitis; conjunctivitis; bronchial asthma;

OS beta-chemokine receptor; viral infection.

SW Homo sapiens.

PN WO9741154-A1.

PD 06-NOV-1997.

PF 24-APR-1997; U065568.

PR 17-JAN-1997; GB-000894.

PR 26-APR-1996; US-016158.

PR 26-APR-1996; US-017113.

PA (MERI) MERCK & CO INC.

PI Daugherty BL, Demartino JA, Siciliano SJ, Springer MS;

DR WPI: 97-549685/50.

DR N-PSDB; T93601.

PT New isolated human eosinophil eotaxin receptor - used to develop

PT products for treating and preventing atopic conditions e.g. allergic

PT rhinitis, dermatitis, conjunctivitis and bronchial asthma

PS Claim 5; Page 15; 51pp; English.

CC This is a human eosinophil eotaxin receptor. The 5099 base pair encoding

CC cDNA sequence comprises a 1065 base pair open reading frame encoding this

CC 355 amino acid eosinophil eotaxin receptor protein, flanked by a 5'

CC genomic DNA sequence and a 3' terminator region. This novel eosinophil

CC eotaxin receptor is a human beta-chemokine receptor designated CC CCR3.

CC Agents which bind to this eosinophil eotaxin receptor can be used for

CC the treatment and prevention of atopic conditions such as allergic

CC rhinitis, dermatitis, conjunctivitis and bronchial asthma. Agents which

CC block this eosinophil eotaxin receptor can be used to prevent viral

CC infection in healthy individuals and slow or halt viral progression

CC in infected patients.

SQ Sequence 355 AA;

Query Match 100.0%; Score 2760; DB 28; Length 355;

Best Local Similarity 100.0%; Pred. No. 2.88e-228;

Matches 355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 mttsltdvtetgtsyddvgllceakdralmagfpvplyslvftvgllgnvvwmil 60

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QY 1 MTTSLDTVETGTTSSYYDDVGLLCEKADTRALMAQFVPLLSLVFTVGLGNVVMVMI 60
Db 61 KyrllrImtniYllnlaISdlflvtlpfwhvgrhwnvfgbmcKllsgfyhtglyse 120
QY 61 KYRRLRIMTNIYLLNLAIISDLFLVTLFPWHVYGRHWNVFGHGMCKLLSGFYHTGLYSE 120
Db 121 IffilllIdrylaivhavfalrartvfgvitsvltwglavlaalpefifeteelfee 180
QY 121 IFFIILLIDRYLAIVHAVFALRARTVFGVITSVLTWGLAVLAALPEFIFYETEELFEE 180
Db 181 tlcsalypedvyswrhfhltlrmfclvpllvmaicytgiktlrcpskkykairl 240
QY 181 TLCSALYPEDVYSWRHFHTLRTMIFCLVPLLVMAICYTGIIKTLRCPSKKYKAIRL 240
Db 241 Ifvimavffifwtpynvaillssyqsilfgndcerskhldlvmlyteviayshccmpvi 300
QY 241 IFVIMAVFFIETWPNVAILSSYQSILFGNDCERSKHLDLVMLVTEVIAYSHCCMPVI 300
Db 301 yafvgerfrkylrhffhrlhmlgryipflpsekletssvstaeplsivf 355
QY 301 YAFVGERFRKYLRFHFRHLLHMLGRYIPFLPSEKLETSVSSPSTAEPLSIVF 355

ID W2124 standard; Protein; 355 AA.
AC W2124;
DE 14-DEC-1997 (first entry)
DE Human chemokine receptor 88-2B.
KW Chemokine receptor 88-2B; atherosclerosis; rheumatoid arthritis;
KW tumour; asthma; viral infection; AIDS; inflammation;
KW autoimmune disease; therapy; diagnosis; leukocyte trafficking;
KW G protein coupled receptor; ligand; modulator; antibody; human.
OS Homo sapiens.
FH Key Location/Qualifiers
FT domain 1..36
FT /label= Extracellular_domain
FT domain 60..71
FT /label= Intracellular_domain
FT domain 93..107
FT /label= Extracellular_domain
FT domain 131..151
FT /label= Extracellular_domain
FT domain 171..196
FT /label= Extracellular_domain
FT domain 219..240
FT /label= Intracellular_domain
FT domain 263..284
FT /label= Extracellular_domain
FT domain 306..355
FT /label= Intracellular_domain

W09722698-A2.
26-JUN-1997.
PF 26-DEC-1996; U20759.
PR 07-JUN-1996; US-661393.
PR 20-DEC-1995; US-575967.
PA (ICOS-) ICOS CORP.
PI Gray PW, Raport CJ, Schweickart VL;
PI WPI: 97-341689/31.
DR N-PSDB: T85162.
PT New nucleic acid encoding chemokine receptors 88-2B and 88C - used
PT to modulate leukocyte trafficking, e.g. for treatment of
PT inflammation, tumours, viral infections, autoimmune diseases, etc.
PS Claim 1; Page 50-51; 65pp; English.
CC This polypeptide sequence comprises novel human chemokine receptor
CC 88-2B, a G protein coupled receptor that is involved in leukocyte
CC trafficking. Its amino sequence was deduced from a cDNA clone
CC (T85162) isolated from a macrophage library. It shows 72% identity
CC to CCKR1. Chemokine receptor 88C (see W2123) has also been
CC identified. 88C and 88-2B receptors and their polypeptide fragments
CC can be produced in transformed host cells. The receptors, peptides
CC comprising one or more of the extracellular or intracellular
CC domains, and anti-receptor antibodies can be used to modulate
CC receptor activities, particularly ligand and G protein binding, and
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CC are potentially potentially useful in the treatment of
CC atherosclerosis, rheumatoid arthritis, tumours, asthma, viral
CC infection, AIDS, inflammatory conditions, pathological immune
CC response, abnormal haematopoietic processes etc.
SQ Sequence 355 AA;

Query Match 100.0%; Score 2760; DB 24; Length 355;
Best Local Similarity 100.0%; Pred. No. 2.88e-228;
Matches 355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 mttSLDTVETGTTSSYYDDVGLLCEKADTRALMAQFVPLLSLVFTVGLGNVVMVMI 60
QY 1 MTTSLDTVETGTTSSYYDDVGLLCEKADTRALMAQFVPLLSLVFTVGLGNVVMVMI 60
Db 61 KyrllrImtniYllnlaISdlflvtlpfwhvgrhwnvfgbmcKllsgfyhtglyse 120
QY 61 KYRRLRIMTNIYLLNLAIISDLFLVTLFPWHVYGRHWNVFGHGMCKLLSGFYHTGLYSE 120
Db 121 IffilllIdrylaivhavfalrartvfgvitsvltwglavlaalpefifeteelfee 180
QY 121 IFFIILLIDRYLAIVHAVFALRARTVFGVITSVLTWGLAVLAALPEFIFYETEELFEE 180
Db 181 tlcsalypedvyswrhfhltlrmfclvpllvmaicytgiktlrcpskkykairl 240
QY 181 TLCSALYPEDVYSWRHFHTLRTMIFCLVPLLVMAICYTGIIKTLRCPSKKYKAIRL 240
Db 241 Ifvimavffifwtpynvaillssyqsilfgndcerskhldlvmlyteviayshccmpvi 300
QY 241 IFVIMAVFFIETWPNVAILSSYQSILFGNDCERSKHLDLVMLVTEVIAYSHCCMPVI 300
Db 301 yafvgerfrkylrhffhrlhmlgryipflpsekletssvstaeplsivf 355
QY 301 YAFVGERFRKYLRFHFRHLLHMLGRYIPFLPSEKLETSVSSPSTAEPLSIVF 355

RESULT 3
ID W03377 standard; Protein; 355 AA.
AC W03377;
DE 15-NOV-1996 (first entry)
DE CC-chemokine receptor 3.
DE CC-chemokine receptor 3; CKP-3; Eos-L2; inhibitor; antisense;
KW antinflammatory; eosinophil.
OS Homo sapiens.
FH Key Location/Qualifiers
FT region 130..138
FT /note= "amino acids 130-138 comprise a motif
FT conserved among C-X-C and C-C chemokine
FT receptors".
PN W09622371-A2.
PD 25-JUL-1996.
PR 19-JAN-1996; U00608.
PR 19-JAN-1995; US-375199.
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.
PA (CHIL-) CHILDRENS MEDICAL CENT.
PA (LEUK-) LEUKOSITE INC.
PI Gerard CJ, Gerard NP, Mackay CR, Ponath PD, Post TW;
PI Qin S;
PI WPI: 96-354528/35.
DR N-PSDB: T31335.
PT Mammalian chemokine receptor-3 and related nucleic acids - useful to
PT identify receptor inhibitors to treat inflammatory disease, e.g.
PT autoimmune disorders, certain cancers, etc.
PS Claim 10; Page 113-114; 153pp; English.
CC A novel human receptor (W03377), designated Eos L2 or C-C chemokine
CC receptor 3 (CKR-3), is involved in leukocyte migration associated
CC with inflammation. Its sequence was deduced from a cDNA clone
CC (T31335) isolated from a hyper-eosinophilic syndrome patient. A
CC slightly different amino acid sequence (W03376) was deduced from a
CC genomic clone (T31334) and a consensus sequence is given in W03378.
CC Recombinant CKR-3 can be produced in host cells, and is useful for
CC screening for CKR-3 ligands, promoters and inhibitors. The
CC inhibitors can be used to treat inflammatory disease.
SQ Sequence 355 AA;
```

Query Match 100.0%; Score 2760; DB 19; Length 355;
 Best Local Similarity 100.0%; Pred. No. 2.88e-228;
 Matches 355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 mtsldtvetftgtsydvddgllcekadtralmqfvpplyslvfvgllgnvnmvmlil 60
 QY 1 MTSLSDTVETFTGTSYDVDDGLLCEKADTRALMAQFVPPPLYSLVFVGLLGNVNMVMI 60

Db 61 kyrirrimtniylnlaisdlflvltplfwihyvrghnvwfghgmckllsgfyhtglyse 120
 QY 61 KYRRLRIMTNIYLLNLAISDLLFLVLTPLFWIHVYRGHNWVFGHGMCKLLSGFYHTGLYSE 120

Db 121 iffiilltldrylaivhavfalrartvtfgvitsvtwglavlaalpefifeteelfee 180
 QY 121 IFIILLTLDRYLAIVHAVFALRARTVTFGVITSVTWGLAVLAALPEFIFETEELFEE 180

Db 181 tlcsalypedtvyswrhftlmtlfcvlpplvmaicvtgiiktllrcpskkkykairl 240
 QY 181 TLCSALYPEDTVYSWRHFTRLMTLFCVLPPLVMAICVTGIKTLRLCPSKKKYKAIRL 240

Db 241 ifvimaaffwtpynvnaillssyqilfgndcerskhldlvmvltvteiyashccmnpvi 300
 QY 241 IFVIMAFFWTPYNVNAILLSSYQILFGNDCERSKHLDLVMTVEVIYASHCCMNPVI 300

Db 301 yafvgerfkyrlrhffrhlmlhgrlyipflpseklertssvpspaeplsivf 355
 QY 301 YAFVGERFRKYLRFHFRHLLMHLGRYIPFLPSEKLERTSVSSPSPAEPLSIVF 355

RESULT 4

ID W10100 standard; Protein: 355 AA.

AC W10100;
 DT 30-SEP-1997 (first entry)
 DE Human C-C chemokine receptor 3.
 KW Human; eotaxin; eosinophil; chemoattractant; stimulation;
 KW accumulation; attraction; chemotaxis; diagnosis; prevention;
 KW treatment; disease; inflammation; allergy; asthma; rhinitis;
 KW hypersensitivity; lung; pneumonia; Loeffler's; syndrome;
 KW interstitial; ILD; idiopathic pulmonary fibrosis;
 KW rheumatoid arthritis; systemic; lupus erythematosus; SLE;
 KW ankylosing spondylitis; sclerosis; Sjogren's; polymyositis;
 KW dermatomyositis; bowel; anaphylaxis; drug; penicillin;
 KW cephalosporin; insect sting; Crohn's; ulcerative colitis;
 KW spondyloarthropathy; scleroderma; psoriasis; dermatosis;
 KW vasculitis; eczema; atopic; urticaria; necrotizing; cutaneous;
 KW myasthenia gravis; juvenile onset diabetes; glomerulonephritis;
 KW autoimmune; thyroiditis; Bechet's; graft; rejection;
 KW transplantation; allograft; graft versus host; cancer;
 KW leukocyte infiltration; reperfusion injury; atherosclerosis;
 KW haematologic malignancy; septic; endotoxemic; shock;
 KW polymyositis; dermatomyositis; immunosuppression; immunodeficiency;
 KW AIDS; radiation therapy; chemotherapy; autoimmune; corticosteroid;
 KW C-C chemokine receptor 3; CRK3.
 OS Homo sapiens.
 PN MO9700960-A1.
 PN 09-JAN-1997.
 PF 21-JUN-1996; U10723.
 PR 23-JUN-1995; US-494093.
 PA (LEUK-) LEUKOSTE INC.
 PI Mackay C, Newman W, Ponath PD, Qin S, Ringler DJ;
 DR N-PSDB; T58783.
 DR New isolated human eotaxin gene - used to develop prods. for the
 PT diagnosis and treatment of e.g. inflammation, allergies, auto-immune
 PT disease, infections and tumours
 PS Example 7; Pages 98-99; 130pp; English.
 CC The present sequence is human C-C chemokine receptor 3 (CRK3),
 CC to which human eotaxin (hE), an eosinophil specific chemoattractant
 CC capable of stimulating eosinophil accumulation and/or attracting
 CC eosinophils (including chemotaxis), binds.
 CC hE can be used to develop products for the diagnosis, prevention or

CC treatment of hE associated diseases or conditions. The products can
 CC be used to treat inflammatory or allergic diseases and conditions,
 CC including respiratory allergic diseases (e.g. asthma, allergic
 CC rhinitis, hypersensitivity lung diseases or pneumonitis,
 CC eosinophilic pneumonia such as Loeffler's syndrome and chronic
 CC eosinophilic pneumonia, interstitial lung diseases (ILD) such as
 CC idiopathic pulmonary fibrosis or ILD associated with rheumatoid
 CC arthritis, systemic lupus erythematosus (SLE), ankylosing
 CC spondylitis, systemic sclerosis, Sjogren's syndrome, polymyositis
 CC or dermatomyositis), systemic anaphylaxis or hypersensitivity
 CC responses, drug allergies (e.g. to penicillin and cephalosporins),
 CC insect sting allergies, inflammatory bowel diseases (e.g. Crohn's
 CC disease and ulcerative colitis), spondyloarthropathies,
 CC scleroderma, psoriasis and inflammatory dermatoses (e.g.
 CC dermatitis, eczema, atopic dermatitis, allergic contact dermatitis,
 CC urticaria and necrotizing, cutaneous and hypersensitivity
 CC vasculitis), eosinophilic myositis and fascitis, multiple
 CC sclerosis, SLE, myasthenia gravis, juvenile onset diabetes,
 CC glomerulonephritis, autoimmune thyroiditis, Bechet's disease, graft
 CC rejection (e.g. in transplantation) including allograft rejection or
 CC graft versus host disease and cancers with leukocyte infiltration
 CC of the skin or organs. The products can also be used to treat other
 CC diseases or conditions requiring the inhibition of undesirable
 CC inflammatory responses, including reperfusion injury.
 CC atherosclerosis, certain haematologic malignancies, cytokine
 CC induced toxicity (e.g. septic or endotoxic shock), polymyositis,
 CC dermatomyositis, immunosuppression (e.g. in individuals with
 CC immunodeficiency syndromes such as AIDS, undergoing radiation
 CC therapy, chemotherapy, therapy for autoimmune disease or other drug
 CC therapy, such as corticosteroid therapy, which causes
 CC immunosuppression), immunosuppression due to (e.g. congenital)
 CC deficiency (e.g. in eotaxin) or infectious diseases such as parasitic
 CC diseases.

CC Sequence 355 AA;

Query Match 99.9%; Score 2758; DB 23; Length 355;
 Best Local Similarity 99.7%; Pred. No. 4.32e-228;
 Matches 354; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 mtsldtvetftgtsydvddgllcekadtralmqfvpplyslvfvgllgnvnmvmlil 60
 QY 1 MTSLSDTVETFTGTSYDVDDGLLCEKADTRALMAQFVPPPLYSLVFVGLLGNVNMVMI 60

Db 61 kyrirrimtniylnlaisdlflvltplfwihyvrghnvwfghgmckllsgfyhtglyse 120
 QY 61 KYRRLRIMTNIYLLNLAISDLLFLVLTPLFWIHVYRGHNWVFGHGMCKLLSGFYHTGLYSE 120

Db 121 iffiilltldrylaivhavfalrartvtfgvitsvtwglavlaalpefifeteelfee 180
 QY 121 IFIILLTLDRYLAIVHAVFALRARTVTFGVITSVTWGLAVLAALPEFIFETEELFEE 180

Db 181 tlcsalypedtvyswrhftlmtlfcvlpplvmaicvtgiiktllrcpskkkykairl 240
 QY 181 TLCSALYPEDTVYSWRHFTRLMTLFCVLPPLVMAICVTGIKTLRLCPSKKKYKAIRL 240

Db 241 ifvimaaffwtpynvnaillssyqilfgndcerskhldlvmvltvteiyashccmnpvi 300
 QY 241 IFVIMAFFWTPYNVNAILLSSYQILFGNDCERSKHLDLVMTVEVIYASHCCMNPVI 300

Db 301 yafvgerfkyrlrhffrhlmlhgrlyipflpseklertssvpspaeplsivf 355
 QY 301 YAFVGERFRKYLRFHFRHLLMHLGRYIPFLPSEKLERTSVSSPSPAEPLSIVF 355

RESULT 5
 ID W03376 standard; Protein: 355 AA.


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Db 59 lvqvkrlkmtsiylnlaisdlflftlplfwidylkddwvfgdamckllsgfyytgly 118
Qy 59 LIKVRRLRIMTNIYLLNLAISDLFLVLPFWIHVVRGHNWVFGHGMCKLLSGFYHTGLY 118
Db 119 seiffilltdrylaihvafalrartvtfgvitsiilwalailasmpglyfsktgwe 178
Qy 119 SEIFFIILLTDRLYLAIHVAFALRARTVTFGVITSIVTWGLAVLAALPEFIFYETEELF 178
Db 179 thtcslhphesirewklfgalnlfglplvlmlicygtgikillrrpnekkaskav 238
Qy 179 BETLCSALYPEDTVYSWRHFHTLMTIFCLVPLLVMAICYTGIIKTLRCPSSKKYKAI 238
Db 239 rlfvimiiffitpynltlilsvfdqflftheceqsrhldlavqvtviaythccvnp 298
Qy 239 RLIFVIMAVFFIWTPTYNVAILLSYOSILFGNDCERSKHLDLVNLVTEVAYSHCCMNP 298
Db 299 viyafvgerfrkylrqlfhrvavhlvkwplfslvdrlervsstpspstegehelsagf 355
Qy 299 VIYAFVGERFRKYLHRHFHRLHMLGRYIPLPSEKLERISSVSPSTABPELSIVF 355
Db 239 rlfvimiiffitpynltlilsvfdqflftheceqsrhldlavqvtviaythccvnp 298
Qy 239 RLIFVIMAVFFIWTPTYNVAILLSYOSILFGNDCERSKHLDLVNLVTEVAYSHCCMNP 298
Db 299 viyafvgerfrkylrqlfhrvavhlvkwplfslvdrlervsstpspstegehelsagf 355
Qy 299 VIYAFVGERFRKYLHRHFHRLHMLGRYIPLPSEKLERISSVSPSTABPELSIVF 355
RESULT 10
ID W25751 standard; Protein; 355 AA.
AC W25751;
DT 20-NOV-1997 (first entry)
DE Human MIP-1alpha/RANTES receptor protein.
KW Human MIP-1 alpha/RANTES receptor; osteoporosis; pCCR; digestive ulcer;
KW macrophage inflammatory protein 1 alpha; diabetes; central disease;
KW regulated on activation, normal T cell expressed and secreted; allergy;
KW affinity compound; expression vector; CHO cell; viral disease;
KW infectious disease; tumour; hyperlipidaemia; hypercholesterolaemia.
OS Homo sapiens.
PN J09176048-A.
PF 28-DEC-1995; 342130.
PR 28-DEC-1995; JP-342130.
PA (TAKE ) TAKEDA CHEM IND LTD.
DR WPI; 97-399449/37.
DR N-PSDB; T86154.
PT Preparation of human MIP-1-alpha/RANTES receptor protein - used in
PT the treatment of viral diseases, tumours, allergy, diabetes
PT osteoporosis etc.
PS Disclosure; Page 15-16; 19pp; Japanese.
CC This sequence represents human MIP-1 alpha/RANTES receptor (macrophage
CC inflammatory protein 1 alpha/regulated on activation, normal T cell
CC expressed and secreted). The human MIP-1 alpha/RANTES receptor protein
CC may be used in a method for the screening of human MIP-1 alpha/RANTES
CC receptor affinity compounds. The MIP-1 alpha/RANTES receptor coding
CC sequence may be included in an expression vector, preferably pCCR, and
CC used to transform a CHO cell for use in the same method. The receptor
CC protein can provide a preventive and treating agent for viral diseases,
CC infectious diseases, tumours, allergy, diabetes, central diseases,
CC hyperlipidaemia, hypercholesterolaemia, osteoporosis, digestive ulcers,
CC etc.
SQ Sequence 355 AA;
Query Match 66.4%; Score 1834; DB 24; Length 355;
Best Local Similarity 63.0%; Pred. No. 1.32e-146;
Matches 225; Conservative 67; Mismatches 61; Indels 4; Gaps 4;
Db 1 metp-nttedydttefogydatp-cqkvnerafagallpplvslvfgilvgailvvlv 58
Qy 1 MTTSLDVTVEFTGTS-Y-YDDVGLCEKADTRALMAQFVPLYSLVFTVGLGNVVMYI 58
Db 59 lvqvkrlkmtsiylnlaisdlflftlplfwidylkddwvfgdamckllsgfyytgly 118
Qy 59 LIKVRRLRIMTNIYLLNLAISDLFLVLPFWIHVVRGHNWVFGHGMCKLLSGFYHTGLY 118
Db 119 seiffilltdrylaihvafalrartvtfgvitsiilwalailasmpglyfsktgwe 178
Qy 119 SEIFFIILLTDRLYLAIHVAFALRARTVTFGVITSIVTWGLAVLAALPEFIFYETEELF 178
Db 179 thtcslhphesirewklfgalnlfglplvlmlicygtgikillrrpnekkaskav 238

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Qy 179 BETLCSALYPEDTVYSWRHFHTLMTIFCLVPLLVMAICYTGIIKTLRCPSSKKYKAI 238
Db 239 rlfvimiiffitpynltlilsvfdqflftheceqsrhldlavqvtviaythccvnp 298
Qy 239 RLIFVIMAVFFIWTPTYNVAILLSYOSILFGNDCERSKHLDLVNLVTEVAYSHCCMNP 298
Db 299 viyafvgerfrkylrqlfhrvavhlvkwplfslvdrlervsstpspstegehelsagf 355
Qy 299 VIYAFVGERFRKYLHRHFHRLHMLGRYIPLPSEKLERISSVSPSTABPELSIVF 355
RESULT 11
ID W29179 standard; Protein; 355 AA.
AC W29179;
DT 19-DEC-1997 (first entry)
DE Rat CC chemokine receptor.
KW Rat; CC chemokine receptor; screen; binding; ligand.
OS Rattus rattus.
PN J09227599-A.
PF 02-SEP-1997.
PR 22-FEB-1996; 035192.
PA (TAKE ) TAKEDA CHEM IND LTD.
DR WPI; 97-486426/45.
DR N-PSDB; T86839.
PT CC chemokine receptor protein - useful to screen for novel binding
PT compounds
PS Claim 1; Page 20-21; 26pp; Japanese.
CC This sequence is a rat CC chemokine receptor. The receptor can be used
CC to screen for novel binding compounds and for preparation of antibodies
CC or antiserum.
SQ Sequence 355 AA;
Query Match 62.5%; Score 1726; DB 24; Length 355;
Best Local Similarity 57.6%; Pred. No. 4.07e-137;
Matches 205; Conservative 88; Mismatches 61; Indels 2; Gaps 2;
Db 1 meis-nitetypttteydygstpcqktdvrafgallpplvslvfgilvgailvvlv 59
Qy 1 MTTSLDVTVEFTGTSYD-DVGLCEKADTRALMAQFVPLYSLVFTVGLGNVVMYI 59
Db 60 mqhrqlqsmtsiylfnlavsdvlfplfwidylkddwvfgdamckllsgfyytgly 119
Qy 60 IKYRRLRIMTNIYLLNLAISDLFLVLPFWIHVVRGHNWVFGHGMCKLLSGFYHTGLY 119
Db 120 eiffilltdrylaihvafalrartvtfgvitsiilwalailasipalcoffkaqweft 179
Qy 120 EIFIILLTDRLYLAIHVAFALRARTVTFGVITSIVTWGLAVLAALPEFIFYETEELF 179
Db 180 htcsphfpdeslktwkrfgalknlilglilpllmlicyagiirillrrpnekkaskav 239
Qy 180 ETLCSALYPEDTVYSWRHFHTLMTIFCLVPLLVMAICYTGIIKTLRCPSSKKYKAI 239
Db 240 lifailltllftpynltvsvafgdlvfnqceqskldlavqvtviaythccvnp 299
Qy 240 LIFFVIMAVFFIWTPTYNVAILLSYOSILFGNDCERSKHLDLVNLVTEVAYSHCCMNP 299
Db 300 ivyfvgerfrkylrqlfhrvavhlvkwplfslvdrlervsstpspstegehelsagf 355
Qy 300 IYAFVGERFRKYLHRHFHRLHMLGRYIPLPSEKLERISSVSPSTABPELSIVF 355
RESULT 12
ID W27125 standard; Protein; 352 AA.
AC W27125;
DT 14-DEC-1997 (first entry)
DE Macaque chemokine receptor 88C.
KW Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis;
KW tumour; asthma; viral infection; AIDS; inflammation;
KW autoimmune disease; therapy; diagnosis; leukocyte trafficking;
KW G protein coupled receptor; ligand; modulator; antibody.
OS Macaca sp.

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PN WO9722698-A2.
PD 26-JUN-1997.
PF 20-DEC-1996; U20759.
PR 07-JUN-1996; US-661393.
PA (ICOS-) ICOS CORP.
PI Gray PW, Raport CJ, Schweickart VL;
DR WPI; 97-341689/31.
DR N-PSDB; T85163.
PT New nucleic acid encoding chemokine receptors 88-2B and 88C - used
PT to modulate leukocyte trafficking, e.g. for treatment of
PT inflammation, tumours, viral infections, autoimmune diseases, etc.
PS Claim 36; Page 57-58; 65pp; English.
CC This polypeptide sequence comprises macaque chemokine receptor 88C,
CC a G protein coupled receptor that is involved in leukocyte
CC trafficking. Its amino sequence was deduced from a 88C DNA
CC (T85163) isolated by PCR amplification. It shows 97% identity to
CC human 88C (W27123). 88C receptors and their polypeptide fragments
CC can be produced in transformed host cells. The receptors, peptides
CC comprising one or more of the extracellular or intracellular
CC domains, and anti-receptor antibodies can be used to modulate
CC receptor activities, particularly ligand and G protein binding, and
CC are potentially useful in the treatment of
CC atherosclerosis, rheumatoid arthritis, tumours, asthma, viral
CC infection, AIDS, inflammatory conditions, pathological immune
CC response, abnormal haematopoietic processes etc. A hybridoma
CC that produces an antibody that specifically binds to macaque 88C is
CC claimed.
SQ Sequence 352 AA;

      Query Match          54.2%; Score 1497; DB 24; Length 352;
      Best Local Similarity 55.2%; Pred. No. 4.95e-117;
      Matches 185; Conservative 84; Mismatches 57; Indels 9; Gaps 9;

Db 20 cqkinvkqiaarlpplyslvfifgvgnlvlllnckrksmtdiyllnlaisdlif 79
QY 24 CEKADTRALMAQFVPLYSLVFTVGLGNVVMVILIKYRRLRIMNTIYLLNLAISDLF 83

Db 80 lltvpfwahyaaq-wdfgntmcqlltglyfifgffsgifilltldrylavhavfalk 138
QY 84 LVTLPFWIHVYRGNWVFGHGCKLSGYHTGLYSEIFFIILLTIDRYLAIVHAVFALR 143

Db 139 artvtfgvvtvitwvavfaslpglifrsgqreglhyt-csshfysq-yqfwnfqtl 196
QY 144 ARTVFGVITSIVTWGLAVLAALPEFIFETE-ELFEETLCSALYPEDTVYS-WRHFHL 201

Db 197 kmvilglvpllvmycysgilktllrcnrckhravrliftimivylfwapynivil 256
QY 202 RMTIFCLVPLLVMAICYGTGIKTLRCPS-KKKYKAIRLIFVIMAVFFIETPTNVAIL 260

Db 257 lntfqef-fglncssnrlldqamqvteitgmthccinpliyafvgekfrnyllvffqkh 315
QY 261 LSSYQSILFG-NDCCRSKHLDLVLMVTEVIAVSHCCMNPIYAFVGERPKYLRHFHRRH 319

Db 316 iakrfckccsifqgeaperassvyrstgqeqlsv 350
QY 320 LLMHLGRYIPFLPSEKLENTSSV-SPSTAEPPELSI 353

      RESULT 13
      ID W27123 standard; Protein: 352 AA.
      AC W27123.
      DE Human chemokine receptor 88C.
      KW Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis;
      KW tumour; asthma; viral infection; AIDS; inflammation;
      KW autoimmune disease; therapy; diagnosis; leukocyte trafficking;
      KW G protein coupled receptor; ligand; modulator; antibody; human.
      OS Homo sapiens.
      FH Key Location/Qualifiers
      FT domain 1..32
      FT /label= Extracellular_domain
      FT domain 56..67

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FT domain /label= Intracellular_domain
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FT 125..145
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FT 213..235
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FT 259..280
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FT 301..352
FT /label= Intracellular_domain
PN WO9722698-A2.
PD 26-JUN-1997.
PF 20-DEC-1996; U20759.
PR 07-JUN-1996; US-661393.
PA (ICOS-) ICOS CORP.
PI Gray PW, Raport CJ, Schweickart VL;
DR WPI; 97-341689/31.
DR N-PSDB; T85161.
PT New nucleic acid encoding chemokine receptors 88-2B and 88C - used
PT to modulate leukocyte trafficking, e.g. for treatment of
PT inflammation, tumours, viral infections, autoimmune diseases, etc.
PS Claim 16; Page 47-48; 65pp; English.
CC This polypeptide sequence comprises novel human chemokine receptor
CC 88C, a G protein coupled receptor that is involved in leukocyte
CC trafficking. Its amino sequence was deduced from a cDNA clone
CC (T85161) isolated from a macrophage library. It shows 62% identity
CC to CCRK1. Chemokine receptor 88-2B (see W27124) has also been
CC identified. 88C and 88-2B receptors and their polypeptide fragments
CC can be produced in transformed host cells. The receptors, peptides
CC comprising one or more of the extracellular or intracellular
CC domains, and anti-receptor antibodies can be used to modulate
CC receptor activities, particularly ligand and G protein binding, and
CC are potentially useful in the treatment of
CC atherosclerosis, rheumatoid arthritis, tumours, asthma, viral
CC infection, AIDS, inflammatory conditions, pathological immune
CC response, abnormal haematopoietic processes etc.
SQ Sequence 352 AA;

      Query Match          53.8%; Score 1484; DB 24; Length 352;
      Best Local Similarity 54.3%; Pred. No. 6.81e-116;
      Matches 182; Conservative 87; Mismatches 57; Indels 9; Gaps 9;

Db 20 cqkinvkqiaarlpplyslvfifgvgnlvlllnckrksmtdiyllnlaisdlif 79
QY 24 CEKADTRALMAQFVPLYSLVFTVGLGNVVMVILIKYRRLRIMNTIYLLNLAISDLF 83

Db 80 lltvpfwahyaaq-wdfgntmcqlltglyfifgffsgifilltldrylavhavfalk 138
QY 84 LVTLPFWIHVYRGNWVFGHGCKLSGYHTGLYSEIFFIILLTIDRYLAIVHAVFALR 143

Db 139 artvtfgvvtvitwvavfaslpglifrsgqreglhyt-csshfysq-yqfwnfqtl 196
QY 144 ARTVFGVITSIVTWGLAVLAALPEFIFETE-ELFEETLCSALYPEDTVYS-WRHFHL 201

Db 197 kmvilglvpllvmycysgilktllrcnrckhravrliftimivylfwapynivil 256
QY 202 RMTIFCLVPLLVMAICYGTGIKTLRCPS-KKKYKAIRLIFVIMAVFFIETPTNVAIL 260

Db 257 lntfqef-fglncssnrlldqamqvteitgmthccinpliyafvgekfrnyllvffqkh 315
QY 261 LSSYQSILFG-NDCCRSKHLDLVLMVTEVIAVSHCCMNPIYAFVGERPKYLRHFHRRH 319

Db 316 iakrfckccsifqgeaperassvyrstgqeqlsv 350
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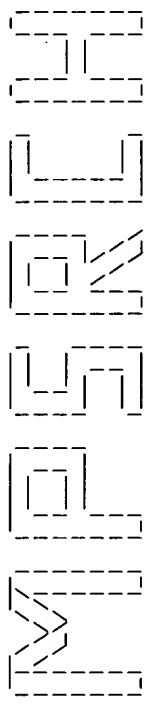
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      ID W27407 standard; Protein: 352 AA.

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Db 257 lntfqef-fglnccssnrlqamqvtetlqnmthccinpiiyafvgekfrnyllvffqkh 315
Qy 261 LSSYQSILFG-NDCCRSKHLDLVMLVTEVIAYSHCCMNPVIYAFYGERFRKYLRRHFHRH 319
Db 316 iakrfckccsifqgeaperassvvtirstgeqeisv 350
Qy 320 LLMLGRYIPFLPSEKLERTSSV-SPSTAPELSI 353

Search completed: Tue Dec 8 13:20:55 1998
Job time : 82 secs.

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(TM)

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ch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Dec 8 23:22:31 1998; MasPar time 1720.66 Seconds
Tabular output not generated. 1527.980 Million cell updates/sec

Title: >US-08-963-656-3
Description: (1-1193) from US08963656.seq
Perfect Score: 1193
N.A. Sequence: 1 TTGTCGCTATCCGGCGAGA.....TTGCCTTAAGAGGAGGACC 1193
Comp: AACACGAATAGCCCGTCT.....AACGGATTCTCCTTCCTGG

Scoring table: TABLE default

Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 567134 seqs, 1101898692 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: emb155
1:em_ba 2:em_fun 3:em_htg 4:em_hum1 5:em_hum2 6:em_in
7:em_om 8:em_or 9:em_ov 10:em_pat 11:em_ph 12:em_pl
13:em_ro 14:em_v1
genbank107
Database:
15:gb_ba1 16:gb_ba2 17:gb_htg 18:gb_in 19:gb_om 20:gb_ov
21:gb_pat 22:gb_ph 23:gb_pl1 24:gb_pl2 25:gb_pr1
26:gb_pr2 27:gb_pr3 28:gb_ro 29:gb_st 30:gb_sts 31:gb_sy
32:gb_un 33:gb_v1

Statistics: Mean 11.128; Variance 4.968; scale 2.240

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1112	93.2	1689	25	HSU49727 Human C-C chemokine re	0.00e+00
2	1110	93.0	1201	27	HSU28694 Human eosinophil CC ch	0.00e+00
3	1110	93.0	1717	25	HSU51241 Human eosinophil eotax	0.00e+00
4	1068	89.5	1068	26	AF036535 Homo sapiens chemokine	0.00e+00
5	962	80.6	1068	26	CAY13775 Cercopithecus aethiops	0.00e+00
6	956	80.1	1068	26	MWY13776 Macaca mulatta CCR-3	0.00e+00
7	952	79.8	1068	26	AF017283 Macaca mulatta chemok	0.00e+00
8	576	48.3	1440	28	MMU28406 Mus musculus macrophag	0.00e+00
9	572	47.9	1185	28	MMU29677 Mus musculus chemokine	0.00e+00
10	562	47.1	1315	28	RNRPKR3 Rattus norvegicus mRNA	0.00e+00
11	555	46.5	1080	28	AF003954 Rattus norvegicus chem	0.00e+00
12	428	35.9	1495	25	HUMCCCKR1A Human C-C chemokine re	0.00e+00
13	428	35.9	1609	21	E13385 cDNA encoding human MI	0.00e+00

Sequence 1 from patent
Homo sapiens macrophag 0.00e+00
Human mRNA for HM145.1 0.00e+00
Macaca mulatta chemok1 0.00e+00
cDNA encoding rat CC c 4.87e-298
Mus musculus macrophag 1.72e-290
Mus musculus chemokine 1.32e-288
Mus musculus macrophag 4.94e-220
Equine herpesvirus 2, 1.48e-212
R.norvegicus mRNA for 6.84e-181
Rattus norvegicus chem 6.84e-181
Mus musculus CC chemok 2.52e-175
House mouse; Musculus 2.52e-175
Macaca nemestrina CC c 2.13e-174
Macaca mulatta chemok1 2.13e-174
Homo sapiens isolate U 1.80e-173
Pan troglodytes isolat 1.52e-172
Mus musculus MIP-1 alp 1.80e-173
Papio hamadryas CC che 1.09e-170
Macaca mulatta CC chem 1.09e-170
Macaca mulatta CC chem 1.09e-170
Papio hamadryas anubis 1.09e-170
Macaca fascicularis CC 1.09e-170
Mus musculus CC chemok 1.09e-170
Cercopithecus aethiops 1.09e-170
Macaca mulatta CC chem 1.09e-170
Pan troglodytes CC che 9.16e-170
Gorilla gorilla CC che 9.16e-170
Homo sapiens isolate M 9.16e-170
Homo sapiens isolate T 9.16e-170
Homo sapiens isolate K 9.16e-170
Homo sapiens isolate U 9.16e-170

ALIGNMENTS

RESULT 1 HSU49727 1689 bp DNA PRI 04-OCT-1996
LOCUS Human C-C chemokine receptor 3 (CKR-3) gene, complete cds.
DEFINITION U49727
ACCESSION
NID g1477560
KEYWORDS human.
SOURCE
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 1689)
AUTHORS Ponath,P.D., Qin,S., Post,T.W., Wang,J., Wu,L., Gerard,N.P.,
Newman,W., Gerard,C. and Mackay,C.R.
TITLE Molecular cloning and characterization of a human eotaxin receptor
expressed selectively on eosinophils
J. Exp. Med. 183 (6), 2437-2448 (1996)
96281895
REFERENCE 2 (bases 1 to 1689)
AUTHORS Ponath,P.D.
TITLE Direct Submission
JOURNAL Submitted (21-FEB-1996) Paul D. Ponath, Molecular Biology,
LeukoSite, Inc., 215 First St., Cambridge, MA 02118, USA
FEATURES
Location/Qualifiers
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ORIGIN

Query Match 93.2%; Score 1112; DB 25; Length 1689;
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Matches 1114; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 78 CAGGAGAGTGAATGACAACTCAGTATAGATACAGTTGAGACCTTTGGTACCACATCCT 137
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Db 227 ACTATGATGACGTGGCCCTGCTCTGAAAAAGCTGTATACAGAGCACTGATGGCCCACT 286
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Qy 138 ACTATGATGACGTGGCCCTGCTCTGAAAAAGCTGTATACAGAGCACTGATGGCCCACT 197
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Db 287 TTGTGCCCCCGCTGACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 346
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Qy 198 TTGTGCCCCCGCTGACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 257
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Db 347 TGATGATCCTCATAAATACAGGAGCTCCGAATTTATGACCAATCTACCTGCTCAACC 406
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Qy 258 TGATGATCCTCATAAATACAGGAGCTCCGAATTTATGACCAATCTACCTGCTCAACC 317
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Db 407 TGGCATTTCGACCTGCTCTTCCTGCTGACCCCTCCATTTGATGATCCTATGTCAGGG 466
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Qy 318 TGGCATTTCGACCTGCTCTTCCTGCTGACCCCTCCATTTGATGATCCTATGTCAGGG 377
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Qy 378 GGCATACTGGGTTTTGGCCATGCGATGTGTAAGTCTCTCAGGGTTTTATCACACAG 437
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Db 527 GCTGTACAGGAGATCTTTTATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 586
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Qy 498 TCCATGCTGTGTTGCCCTTCGAGCCCGGACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 557
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Qy 1038 TCCACAGGCACTTCTCATGACCTGGCGAGATACATCCCATTCCTTCCCTAGTGAAGC 1097
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Db 1187 TGGAAAGAACAGCTCTGCTCTCCATCCACAGCAGCGGAGCACTCTCTATTGTGTTTT 1246
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Db 1247 AGTAGATGCAAAATTCCTTAAGAGGAGGACC 1282
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Qy 1158 AGTAGATGCAAAATTCCTTAAGAGGAGGACC 1193
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RESULT 2

LOCUS HSU28694 1201 bp mRNA PRI 16-MAY-1996
DEFINITION Human eosinophil CC chemokine receptor 3 mRNA, complete cds.
ACCESSION U28694
NID g1199579
KEYWORDS
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Eukaryotes; Metazoa; Chordata;
Vertebrata; Euthera; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 1200)

AUTHORS

Combiere, C., Ahuja, S.K. and Murphy, P.M.

TITLE

Cloning and functional expression of a human eosinophil CC

JOURNAL

J. Biol. Chem. 270 (28), 16491-16494 (1995)

MEDLINE

95348056

REFERENCE

2 (bases 1 to 1201)

AUTHORS

Combiere, C., Ahuja, S.K. and Murphy, P.M.

TITLE

Cloning and functional expression of a human eosinophil CC

JOURNAL

J. Biol. Chem. 271 (18), 11034 (1996)

MEDLINE

96210048

REFERENCE

3 (bases 1 to 1201)

AUTHORS

Combiere, C.

TITLE

Direct Submission

JOURNAL

Submitted (07-JUN-1995) Christophe Combadiere, NIAID, National
Institutes of Health, Building 10, Room 1111, Bethesda, MD 20892,
USA

COMMENT

On Feb 22, 1996 this sequence version replaced gi:881569.

FEATURES

Location/Qualifiers

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CDS

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BASE COUNT 278 a 320 c 267 g 336 t

ORIGIN

Query Match 93.0%; Score 1110; DB 27; Length 1201;
Best Local Similarity 99.9%; Pred. No. 0.00e+00;
Matches 1116; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy 78 CAGGAGAGTGAATGACAACTCAGTATAGATACAGTTGAGACCTTTGGTACCACATCCT 137
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Qy	498	TCCATGCTGTGTTTGGCCCTTCGAGCCCGGACTGTCACCTTTTGGTGTGTCATCAGCAGCATCG	557
Db	671	TCACCTGGGGGCGCTGGCAGTGTCTACAGCTCTCTCCTGAAATTTATCTTCTATCAGACTGAAG	730
Qy	558	TCACCTGGGGGCGCTGGCAGTGTCTACAGCTCTCTCCTGAAATTTATCTTCTATCAGACTGAAG	617
Db	731	AGTTGTTTGAAGAGACTCTTTTGCAAGTGTCTTTTACCAGAGAGATACAGTATATAGCTGGA	790
Qy	618	AGTTGTTTGAAGAGACTCTTTTGCAAGTGTCTTTTACCAGAGAGATACAGTATATAGCTGGA	677
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Qy	678	GGCAATTTCCACACTCTGAGAAATGACCATCTTCTGTCTCGTTCTCCCTCTGCTGTTATGG	737
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Qy	738	CCATCTGCTACACAGGAATCATCAAAAGCTGTGAGTGCCTCCAGTAAAAAAGTACA	797
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Db	1091	TGAACCCGGTGATCTAGCCCTTTTGTGAGAGAGGTTCCGGGAAGTACCTGCGCCACTTCT	1150
Qy	978	TGAACCCGGTGATCTAGCCCTTTTGTGAGAGAGGTTCCGGGAAGTACCTGCGCCACTTCT	1037
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Qy	1038	TCCACAGGCAGTCTGCTATGACACCTGGGCAGATACATCCCATCTTCTTCTAGTGAGAGC	1097
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DEFINITION	Homo sapiens chemokine receptor (CCR3) mRNA, complete cds.		
ACCESSION	AF026535		
NID	G2582565		
KEYWORDS	human.		
SOURCE	Homo sapiens		
ORGANISM	Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;		
REFERENCE	Primates; Catarrhini; Hominoidea; Homo.		
AUTHORS	1 (bases 1 to 1068)		
TITLE	Xiao, L., Weiss, S., Qari, S., Rudolph, D., Hodge, T. and Lal, R.		
JOURNAL	Partial resistance to infection by syncytium-inducing primary HIV-1		
REFERENCE	in exposed uninfected individuals homozygous for CCR5 32bp deletion		
AUTHORS	Unpublished		
TITLE	2 (bases 1 to 1068)		
JOURNAL	Qari, S.		
REFERENCE	Direct Submission		
TITLE	Submitted (24-SEP-1997) Retrovirus Diseases Branch, Centers for		
JOURNAL	Disease Control and Prevention, 1600 Clifton Road, Atlanta, GA		

QY 1112 TCTGTCTCTCCATCCACAGAGAGCCGGAAGTCTCTATGTGTTTAG 1159

RESULT 6 MMV13776 1068 bp DNA PRI 16-FEB-1998
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 DEFINITION Y13776
 ACCESSION 92266685
 NID C-C chemokine receptor-3; CCR-3 gene.
 KEYWORDS rhesus monkey.
 SOURCE Macaca mulatta
 ORGANISM Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
 Primates; Catarrhini; Cercopithecoidea; Cercopithecoidea; Macaca.
 REFERENCE 1 (bases 1 to 1068)
 AUTHORS Sol,N., Treboute,C., Gomas,E., Ferchal,F., Shacklett,B. and
 Alizon,M.
 TITLE The rhesus macaque CCR3 chemokine receptor is a cell entry cofactor
 for HIV-2, but not for HIV-1
 JOURNAL Virology 240 (2), 213-220 (1998)
 MEDLINE 98118446
 REFERENCE 2 (bases 1 to 1068)
 AUTHORS Alizon,M.
 TITLE Direct Submission
 JOURNAL Submitted (12-JUN-1997) M. Alizon, Institut Cochin de Genetique
 Moleculaire, ICM, 22 rue Mechain, 75014 Paris, FRANCE
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gene

CDS

Query Match 80.1%; Score 956; DB 26; Length 1068;
 St Local Similarity 94.8%; Pred. No. 0.00e+00;
 Matches 1012; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

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 Db 61 GGCCTGCTCTGTGAAAAGCCGATGTCGGAGCAGTATGATGATGATGATGATGATG 120
 QY 152 GGCCTGCTCTGTGAAAAGCCGATGTCGGAGCAGTATGATGATGATGATGATGATG 211
 Db 121 TATTCCTGGTTCATGGTGGGCTCTTGGGCAACGTGGTGGTGGTGGTGGTGGTGGT 180
 QY 212 TACTCCCTGGTTCATGGTGGGCTCTTGGGCAACGTGGTGGTGGTGGTGGTGGTGGT 271
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Db 301 TTCAGCCATGGCATGTGTAAGTCTCTCTCGGGTTTTTATCACACAGAGCTTGTACAGCGAG 360
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 Db 361 ATCTTTTTCATATCCCTCCCTGACGATTGACAGGTACCTGGCCATTGCTCCATGCTGTTT 420
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 Db 781 ATCTCTACCTATCAATCCGCTTTATTTGGACTGTGAAAGGAGCAAGCATCTGGAC 840
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 QY 932 CTGTTCTGTCTGGGAGGAGTATGCGCTACTCTCCACTGCTGCGTGAACCCAGTATC 991
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 DEFINITION Macaca mulatta chemokine receptor (CCR3) gene, complete cds.
 ACCESSION AF017283
 NID 92407218
 KEYWORDS rhesus monkey.
 SOURCE Macaca mulatta
 ORGANISM
 REFERENCE 1 (bases 1 to 1068)
 AUTHORS Hauer,D.A., Margulies,B.J. and Clements,J.E.
 TITLE Direct Submission
 JOURNAL Submitted (05-AUG-1997) Division of Comparative Medicine, Johns
 Hopkins University School of Medicine, 720 Rutland Ave., Traylor
 G-60, Baltimore, MD 21205, USA
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BASE COUNT 229 a 289 c 245 g 305 t
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Best Local Similarity 94.6%; Pred. No. 0.00e+00;
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Qy 392 TTGAGCCATGGCATGTGAAGTCTCTCGGGGTTTTATCACAGGCTGTACAGCCAG 451
Db 361 ATCTTTTTCATATCTCTGACAGTGTGACAGTACCTGGCCATTTGTCATGCTGTGTT 420
Qy 452 ATCTTTTTCATATCTCTGACAGTGTGACAGTACCTGGCCATTTGTCATGCTGTGTT 511
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LOCUS MMU28406 1440 bp DNA ROD 27-FEB-1996
DEFINITION Mus musculus macrophage inflammatory protein-1 alpha receptor-like
2 gene, complete cds.
ACCESSION U28406
NID g1203800
KEYWORDS house mouse.
ORGANISM Mus musculus
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Mus.
REFERENCE 1 (bases 1 to 1440)
AUTHORS Gao, J. L. and Murphy, P. M.
TITLE Cloning and differential tissue-specific expression of three mouse
beta chemokine receptor-like genes, including the gene for a
functional macrophage inflammatory protein-1 alpha receptor
J. Biol. Chem. 270 (29), 17494-17501 (1995)
JOURNAL 95340546
MEDLINE
REFERENCE 2 (bases 1 to 1440)
AUTHORS Gao, J. L.
TITLE Direct Submission
JOURNAL Submitted (05-JUN-1995) Ji-Liang Gao, Lab of Host Defenses, NIAID,
National Institutes of Health, Building 10, Room 11N113, Bethesda,
MD 20892, USA
COMMENT On Feb 27, 1996 this sequence version replaced gi:1199860.
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Matches 820; Conservative 0; Mismatches 244; Indels 0; Gaps 0;

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Db 320 AGAATCAAGAGCTGGGCTCATGCTCCTGCTCACTGTACTCTCCCTGGTGTTCATCATC 379
QY 173 GATACAGAGCACTGATGGCCAGCTTTGTGCCCGCTGTACTCCCTGGTGTTCACGTG 232

Db 380 GGCTCTCTGGCAACATGATGGTGTGTTGATCTCTATAAAGTACAGGAAGCTACAAAT 439
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RESULT 9
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DEFINITION Mus musculus chemokine G-protein-coupled receptor CCR-3 gene,
complete cds.
ACCESSION U29677
NID g1109783
KEYWORDS house mouse.
SOURCE Mus musculus.
ORGANISM Mus musculus; Metazoa; Chordata;
Vertebrata; Euthera; Rodentia; Sciurognathi; Muridae;
Murinae; Mus.
REFERENCE 1 (bases 1 to 1185)
AUTHORS Post,T.W., Bosic,C.R., Rothenberg,M.E., Luster,A.D., Gerard,N. and
Gerard,C.
TITLE Molecular characterization of two murine eosinophil beta chemokine
receptors
JOURNAL J. Immunol. 155 (11), 5299-5305 (1995)
MEDLINE 96072806
REFERENCE 2 (bases 1 to 1185)
AUTHORS Post,T.W., Bosic,C.R., Rothenberg,M.E., Luster,A.D. and Gerard,C.
TITLE Direct Submission
JOURNAL Submitted (21-JUN-1995) Theodore W. Post, Pulmonary, Children's
Hospital, 300 Longwood Ave, Boston, MA 02115, USA
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BASE COUNT 301 a 266 c 249 g 369 t
ORIGIN

Query Match 47.9%; Score 572; DB 28; Length 1185;
Best Local Similarity 76.9%; Pred. No. 0.00e+00;
Matches 818; Conservative 0; Mismatches 246; Indels 0; Gaps 0;

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Db 209 GGCTCTCTGGCAACATGATGTTGTGTTGATCCTCATAAAGTACAGGAAGCTACAAAT 268
QY 233 GGCTCTCTGGCAATGTTGGTGGTGTGATGATCTCTATAAATACAGGAGGCTCCGAAT 292

Db 269 ATGACTAATATCTACTGTTCACTGTGCACTTGGCAATTTCTGACCTGCTCTTCTTCACTGTC 328
QY 293 ATGACCAACATCTACTGCTCAACCTGGCCATTTCCGACCTGCTCTTCTCTGCTCACTCT 352

Db 329 CCATCTCTGATTCACATGTTCTGTGGAATGATGGGTTTTGGCCACTACATGTGCAAA 388
QY 353 CCATCTCTGATTCACATGTTCTGTGGAATGATGGGTTTTGGCCACTACATGTGTAAG 412
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Db	389	ATGCTGTCTGGTGTATTTATTCAGGCTTGTACAGGAGATCTTTTTCATCATCTGCTG	448
QY	413	CTCCTCTCAGGGTTTATCACAGAGCTGTACAGGAGATCTTTTCATCATCTGCTG	472
Db	449	ACAATTGACAGATACCTGGTATGTCCTATGCTGTGTGTCCTTCGAGCCGCACTG	508
QY	473	ACAATGCACAGGACCTGGCCATGTCATGCTGTGTGTCCTTCGAGCCGCACTG	532
Db	509	ACATTTGCTACTACACAGTATCATCTGCGGCTTTCAGGAGCTGGCAGCTGCT	568
QY	533	ACATTTGCTACTACACAGTATCATCTGCGGCTTTCAGGAGCTGGCAGCTGCT	592
Db	569	GAATTTATCTTCCATGAGTCTCAAGACAGCTTTTGGAGAGTTTTCCTGCACTCT	628
QY	593	GAATTTATCTTCTATGAGACTGAAGAGTCTTGAAGAGACTCTTTCGAGCTCT	652
Db	629	CCAGAAGGTGAAGAAGACACTGGAACAGTTTTCATGCTCTAGAGATGAATATCT	688
QY	653	CCAGAAGTACAGTATATAGCTGGAGGCACTTCCACACTCTGAGAATGACCACT	712
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QY	713	CT	772
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QY	773	AGTGCTCCAGTAAAAAAGTACAGGCACTCGGCTCAATTTTGTATGATAGTC	832
Db	809	TTTTTTATTTTGGACCCGCTACAACCTGCTCTCTCTCTCTCTCTCTCTCT	868
QY	833	TTTTTTATTTTGGACCCGCTACAACCTGCTCTCTCTCTCTCTCTCTCTCT	892
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QY	893	TTATTTGGAATGACTGTGAGCGAGCAATCTGACCTGGTGTGCTGCTGACAG	952
Db	929	GTGATGCTTACACCCACTGCTGTGCAACCCAGTATCTACGCTTGTGTGAGAG	988
QY	953	GTGATGCTTACACCCACTGCTGTGCAACCCAGTATCTACGCTTGTGTGAGAG	1012
Db	989	TTCCGGAAGTACCTGCGCTCTTTTCCACAGAAATGAGCAGTTTACCTGGGAA	1048
QY	1013	TTCCGGAAGTACCTGCGCTCTTTTCCACAGGACATCTGCTATGACCTGGCA	1072
Db	1049	ATTCCGTTCTCTGCTGAGAAATGGAAGAACAGTCTGCTCTCCCATCACTGG	1108
QY	1073	ATCCCATCTCTCTGCTGAGAGCTGGAAGAACACCACTGCTCTCTCCATCCA	1132
Db	1109	GAGCAAGAAATCTGTGGTGTGTTTACTTGGCAGAGAAATG	1152
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RESULT	10	NRPCR3 1315 bp mRNA ROD 23-JAN-1998	
LOCUS		Rattus norvegicus mRNA for receptor protein CKR3.	
DEFINITION			
ACCESSION		Y13400	
NID		92814946	
KEYWORDS		receptor protein.	
SOURCE		Norway rat.	
ORGANISM		Rattus norvegicus	
REFERENCE		Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;	
AUTHORS		1 (bases 1 to 1315)	
JOURNAL		Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	
REFERENCE		Harrington, P.M., Newton, D.J., Coleman, J.W. and Flanagan, B.F.	
AUTHORS		Unpublished	
JOURNAL		2 (bases 1 to 1315)	
REFERENCE			
AUTHORS		Direct Submission	
JOURNAL		Submitted (27-MAY-1997) B. Flanagan, University of Liverpool,	
REFERENCE		Department of Immunology, Duncan Building, Daulby Street,	
AUTHORS		University of Liverpool, Liverpool, Merseyside, L69 3GA, UK	
JOURNAL		Revised by [3]	

REFERENCE	3	(bases 1 to 1315)	
AUTHORS		Flanagan, B.	
TITLE		Direct Submission	
JOURNAL		Submitted (23-JAN-1998) B. Flanagan, University of Liverpool,	
COMMENT		Department of Immunology, Duncan Building, Daulby Street,	
FEATURES		University of Liverpool, Liverpool, Merseyside, L69 3GA, UK	
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FEATURES		TWGLAVLAALPEFIFHEQDNFGLSCSPRYGEEDSKRHFALRMIFGLALPLI	
FEATURES		MYCYSGIITLLRCNPKKKHAIQIIFVIMVFIPTVYNLVLISAFHSTFLETS	
FEATURES		COOSIHLDMQVTEVITHCCINPIYAFVGERFKHLRFFHRNVAIYLRKYISF	
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QY	233	GGCTCTTGGCAATCTGGTGTGTGATGATCTCTATAAATACAGGAGCTCCAAAT	292
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QY	413	CTCTCTCAGGGTTTATCACAGGCTTGTACAGGAGATCTTTTTCATCATCTGCTG	472
Db	608	ACAATCGACAGGTACCTGGCTTCATGCTGTGTGGCCCTTCGAGCAGCAACTGTG	667
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Db	668	ACTTTTGTCTATATACAGGATCATCTATGGGGTCTTGGAGATGTTGGAGCACTG	727
QY	533	ACTTTTGTCTATATACAGGATCATCTATGGGGTCTTGGAGATGTTGGAGCACTG	592
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QY	653	CCAGAGGATACAGTATATAGCTGGAGGCAATTTCCACACTCTGAGATGACCACT	712

Db	994	ATTTTCATCTCTCTGGCGCAAACTGGAAGAACACAGCTCTGTCTCCCCATCAACTGGG	1053
Qy	1073	ATCCCATCTCTCTGTAGTGAAGCTGGAAGAACCAGCTCTGTCTCTCCATCCACAGCA	1132
Db	1054	GAGCAAGAAATCTCTGTGTTTTAG	1080
Qy	1133	GAGCGGAACCTCTATTGTGTTTTAG	1159

RESULT	12
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DEFINITION	Human C-C chemokine receptor type 1 (C-C CKR-1) mRNA, complete cds.
ACCESSION	L09230
NID	g179984
KEYWORDS	C-C chemokine receptor type 1.
SOURCE	Homo sapiens cDNA to mRNA.
ORGANISM	Homo sapiens Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 1495)
REFERENCE	Neote,K., DiGregorio,D., Mak,J.Y., Horuk,R. and Schall,T.J. Molecular cloning, functional expression, and signaling characteristics of a C-C chemokine receptor Cell 72 (3), 415-425 (1993)
AUTHORS	
TITLE	
JOURNAL	
MEDLINE	93161416
FEATURES	Location/Qualifiers

[illegible]

Query Match	35.9%	Score 428;	DB 25;	Length 1495;
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Qy	250	GGTGTGTGTATGATCCCTATAAAATACAGAGGCTCCGGAATATGACCAACATCTACT	309	
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Qy	430	TCACACAGGCTGTACACGGAGATCTTTTTTCATATCCTGCTGACAAATCGACAGGTACT	489	
Db	399	GGCCATCGTCCACGCCGCTGTTTGCTTTCGGGGCAGGACCGCTCACTTTTGGTGTCAATCAC	458	

Qy	490	GGCCATTGTCCTATGCCTGTGTTGGCCCTTGCAGCCCGGACTGTCACCTTTGGTGTCATCAC	549
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Db	519	GACCCAATGGGAATTCACATCACCAACCTGCAGCCTTCACCTTTCTCAGCAAGACCCTACG	578
Qy	610	GACTGAGAGTAGTTTGAAGAGAGACTCTTTGGCAGTGCCTTTTACCACGAGGATACAGTATA	669
Db	579	AGAGTGGAAAGCTGTTTTAGCGCTCTGAAACTGAACCTCTTTGGCGTGGTATGTCCTTTGTT	638
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Qy	850	ACCCTACAATGTGGCTATCCTTCTCTCTCTCTCAATCCCATCTTATTTGGAAATGACTG	909
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Qy	910	TGACGGGAGCAAGCATCTGGACCTGGTCATGCTGTGTGACAGAGGTGATCGCCTACTCCCA	969
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Qy	970	CTGCTGATGAACCCGGTGAATCTACGCCCTTTGTTGGAGAGAGGTTCCGGAAGTACCTGCG	1029
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Qy	1030	CCACTTCTTCCAGAGGCATTTGCTCATGCACTGGCGAGATACATCCCATCTCTCTCCTAG	1089
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Qy	1090	TGAGAGCTGGAAAGAACCAAGCTCTGTCTCTCCATCCACACAGCGCGGAACTCTCTAT	1149
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RESULT	13
LOCUS	E13385 1609 bp DNA PAT 27-APR-1998
DEFINITION	cDNA encoding human MIP-1 alpha /RANTES receptor.
ACCESSION	E13385
NID	G3252190
KEYWORDS	JP 1997176048-A/1.
SOURCE	Homo sapiens.
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. 1 (bases 1 to 1609) Honda,S. and Fujisawa,T., PRODUCTION OF HUMAN MIP-1ALPHA/RANTES RECEPTOR PROTEIN AND USE Patent: JP 1997176048-A 1 08-JUL-1997;
REFERENCE	TAKEDA CHEM IND LTD
AUTHORS	OS Homo sapiens (human)
JOURNAL	PN JP 1997176048-A/1 PD 08-JUL-1997
COMMENT	PF 28-DEC-1995 JP 1995342130 PI HONDA SUSUMU, FUJISAWA TOMOYUKI PC A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00, PC A61K45/00, PC A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00, PC A61K45/00, PC A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00, PC C07K14/705,

PC C12N5/10, C12N15/09, C12P21/02, C12Q1/00, (C12P21/02, C12R1.91), PC
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ORIGIN

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Matches 697; Conservative 0; Mismatches 269; Indels 0; Gaps 0;
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Qy 250 GGTGTGTGTATGATCCTCATAAATACAGGAGGCTCCGAATATGACCAACATCTACCT 309
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Qy 370 TGTACGGGGCAATACTGGGTTTGGCCATGGCATGTAAAGTCTCTCTCAGGTTTGA 429
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RESULT 14
LOCUS 158541 2156 bp DNA PAT 14-AUG-1997
DEFINITION Sequence 1 from patent US 5652133.
ACCESSION 158541
NID 92477779
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2156)
AUTHORS Murphy, P.M.
TITLE Cloning and expression of the human macrophage inflammatory protein-1.alpha..alpha.) /rantes receptor
JOURNAL Patent: US 5652133-A 1 29-JUL-1997;
FEATURES
Location/Qualifiers
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BASE COUNT 538 a 547 c 504 g 567 t
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Best Local Similarity 72.2%; Pred. No. 0.00e+00;
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Db 461 GGCCATGCTCCACCGCTGTGTTGCTTGGCGGCAAGGACCTGCTCTCTCTCTCTCTCTCTCT 520
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Db	641	AGAGTGAAGCTTTTCAGGCTCTGAACCTGTAACCTCTTTGGGCTGGTATGCTTTGTT	700
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QY	1150	TGTGTT 1155	
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DEFINITION		Homo sapiens macrophage inflammatory protein-1-alpha/RANTES	
ACCESSION		L10918	
NID		9292416	
KEYWORDS		G-protein activator; G-protein coupled receptor; RANTES receptor; macrophage inflammatory protein-1-alpha.	
SOURCE		Homo sapiens (library: 2 kb HL-60 neutrophil cDNA in lambda-ZAP) cDNA to mRNA.	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Euthera; Primates; Catarrhini; Hominiidae; Homo.	
AUTHORS		Gao J.-L., Tiffany, H.L., Kuhns, D., McDermott, D., Li, X., Francke, U. and Murphy, P.M.	
TITLE		Structure and functional expression of the human macrophage inflammatory protein 1 alpha (MIP-1alpha)/RANTES receptor	
JOURNAL		J. Exp. Med. 177, 1421-1427 (1993)	
MEDLINE		93240122	
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ITGILKILRRPNKSAKRLIFIMIIFFLFWTNYLTLISIVFODFLTFHECEQS			
RHLDAQVTEVIATTHCCVNPVIYAFYGERFKYLRQLFRRVAVHLVKWLPFLSVD			
RLRVSTSPSTGEHLSAGF"			
BASE COUNT	538 a	547 c	504 g
ORIGIN			
Query Match	35.9%	Score 428;	DB 25; Length 2156;
Best Local Similarity	72.2%	Pred. No. 0.00e+00;	
Matches	697;	Conservative	0; Mismatches 269; Indels 0; Gaps 0;
Db	161	GGCCCAACTGCTGCCCCCTCTACTCTCTGTTGGTATTTGTCTATGGCTGGTGGAAACAT	220
QY	190	GGCCCAAGTTTGTGCCCCCTCTACTCTCTGTTGGTATTTGTCTATGGCTGGTGGAAACAT	249
Db	221	CCTGTGGTCTGCTGCTTGTGCAATACAGAGGCTAAAAAATGACCAACATCTACTCT	280
QY	250	GGTGGTGGTATGATCTCTATAAATACAGAGGCTCCGAATATGACCAACATCTACTCT	309
Db	281	CCTGAACCTGGCCATTTCTGACCTGCTTCTCTGTTTACGCTTCCCTTCTGGATCGACTA	340
QY	310	GCTCAACCTGGCCATTTCTGACCTGCTTCTCTGTTTACGCTTCCCTTCTGGATCGACTA	369
Db	341	CAAGTTGAAGGATGACTGGGTTTGGTATGATGCAATGATGATGATGATGATGATGATGAT	400
QY	370	TGTCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	429
Db	401	TTACACAGGCTTGTACAGAGGATCTTTTTCATCTCTGCTGACATTCATGACATGACATGACAT	460
QY	430	TCACACAGGCTTGTACAGAGGATCTTTTTCATCTCTGCTGACATTCATGACATGACATGACAT	489
Db	461	GGCAATGCTCCAGCGGCTGTTTGGCTTGGGCGACGACCGCTCACATTTGGTGTCTATCAT	520
QY	490	GGCAATGCTCCAGCGGCTGTTTGGCTTGGGCGACGACCGCTCACATTTGGTGTCTATCAT	549
Db	521	CAGCATCATCTTTGGGCGCTGCGCATCTTGGCTTCCATCCAGGCTTATCTTTTCCAA	580
QY	550	CAGCATCATCTTTGGGCGCTGCGCATCTTGGCTTCCATCCAGGCTTATCTTTTCCAA	609
Db	581	GACCCCAATGGGAATTCACCTCACACACCTGACGCTTCACTTTTCCATCCAGGCTTATCTTT	640
QY	610	GACTGAAGAGTGTGTAAGAGACTCTTTCAGTGTCTTTTACCCAGAGGATACAGTATA	669
Db	641	AGAGTGAAGCTGTTTTCAGGCTCTGAAACTGAACTTCTTTTGGGCTGGTATTCCTTTGTT	700
QY	670	TAGCTGAGGAGCTTTCACACACTGAGATGACCATCTTCTGCTGCTTCTCCCTCTGCT	729
Db	701	GGTATGATCATCTGTCTACACAGGATTAAGAATTTCTGCTAAGACGACCAAAATGAGAA	760
QY	730	CGTATGGCCATCTGTCTACACAGGATTAAGAATTTCTGCTAAGACGACCAAAATGAGAA	789
Db	761	GAAATCCAAAGCTGTCGGTTGATTTTGTCTCATGATCATCTTTTCTCTTTTGGAC	820
QY	790	AAAGTACAAGGCCATCCGGCTCATTTTGTCTCATGCGGCTTTTTCATTTTCTGGAC	849
Db	821	CCCTTACAATTTGACTATATCTTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	880
QY	850	ACCTTACAATTTGCTATCT	909
Db	881	TGACGAGAGCAGATTTGACCTGGCTGCAAGTGACGAGGCTGATCGCTTACAGCA	940
QY	910	TGACGAGAGCAGATCTGACCTGGCTGCAAGTGACGAGGCTGATCGCTTACAGCA	969
Db	941	CTGCTGTCTCAACCCAGTATCTACGCTTCTGTTTGTGAGAGGTTCCGGAAGTACCTGCG	1000
QY	970	CTGCTGTCTCAACCCAGTATCTACGCTTCTGTTTGTGAGAGGTTCCGGAAGTACCTGCG	1029

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```
ch_nn n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Wed Dec 9 01:11:26 1998; MasPar time 171.85 seconds
          944.517 Million cell updates/sec
Tabular output not generated.
```

Title: >US-08-963-656-3
Description: (1-1193) from US08963656.seq
Perfect Score: 1193
N.A. Sequence: 1 TTGTGCTTATCCGGGCAAGA.....TTGCCTAAAGAGNAGGACC 1193
Comp: AACACGAATAGGCCGGTCT.....AACGGATTTCTCCTCTCGG

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 188442 seqs, 68026449 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

```
Database:
n-geneseq32
1:part8 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part9 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39 40:part40
```

Statistics: Mean 9.178; Variance 5.134; scale 1.788

Pred: No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query %			ID	Description	Pred. No.
	Score	Match	Length			
1	1193	100.0	1193 23	T31335	CC-chemokine receptor	0.00e+00
2	1112	93.2	1116 33	T31336	CC-chemokine receptor	0.00e+00
3	1112	93.2	1689 32	T58783	Human C-C chemokine r	0.00e+00
4	1112	93.2	1689 23	T31334	CC-chemokine receptor	0.00e+00
5	1110	93.0	1915 34	T85162	Human chemokine recep	0.00e+00
6	1110	93.0	5099 38	T35601	Human eosinophil eota	0.00e+00
7	1034	86.7	1071 36	T79096	Human CCR3 chemokine	0.00e+00
8	428	35.9	1065 33	T86154	Human MIP-1alpha/RAN	1.28e-295
9	428	35.9	1495 11	Q62695	C-C chemokine recepto	1.28e-295
10	428	35.9	2156 34	T50384	Human MIP-1 alpha/RAN	1.28e-295
11	359	30.1	1534 34	T86839	cDNA encoding rat CC	3.21e-243
12	223	18.7	1059 34	T85163	Macaque chemokine rec	8.30e-141
13	220	18.4	1225 39	T76920	DNA encoding human CC	1.44e-138


```

QY 258 TGATGATCCTCATAAAATACAGAGGCTCGGAATTATGACCAACATCTACCTGCTCAACC 317
Db 241 tggccatttggaccctgtcttctcgtcaaccctccattccttgatccaccatgtcaggg 300
QY 318 TGCCCAATTCGGACCTGCTCTTCTCGTCAACCTTCCATTTCTGGATCCACTATGTGAGG 377
Db 301 ggcataactgggttttggccatggcatgtgaagctccctcagggttttatcacacag 360
QY 378 GGCATAACTGGGTTTTGGCCATGGCATGTGTAGCTCTCTCAGGGTTTTATCACACAG 437
Db 361 gctttacacagcagatctttttcataatccctgtctgacaatcgacagtgactcggccattg 420
QY 438 GCITGTGACACGAGATCTTTTTCATATCTCTGCTGACATCGACAGGTACTCGGCCATTG 497
Db 421 tccatgctgtgttgccttcgagccggagctgtcaacttttgggtgtaaccacagatcg 480
QY 498 TCCATGCTGTGTTTGGCCTTCGAGCCGGAGCTGTCACTTTTGGTGTGATCACCAGCATCG 557
Db 481 tcacctgggscctggcagtgactagcagctcttctgaatttcttctatgagactgaag 540
QY 558 TCACCTTGGGGCCTTGGCAGTCTAGCAGCTCTTCTGGAATTTATCTTATGAGACTGAAG 617
Db 541 agttgtttgaagactcttttgcagtgctctttaccacagaggatcacagtatatgctgga 600
QY 618 AGTGTGTTGAAGAGACTCTTTTGCAGTGCTCTTACCACAGAGATACAGTATATAGCTGA 677
Db 601 gssatttccacactctgagaaatgacacatctctgtctgtcttccctcctcgtctgtatgg 660
QY 678 GGCATTTCCACACTCTGAGAAATGACCATCTCTGCTCTGCTTCTCCCTCTGCTGTTATGG 737
Db 661 ccactgctacacaggaatcatcaaacgctgctgaggtgcccagtaaaaaagataca 720
QY 738 CCATCTGCTACACAGGAATCATCAAAACGCTGCTGAGGTGCCCGAGTAAAAAAGTACA 797
Db 721 aggccatccggctcatttttgcatactgctgggtgtttttcattttctgtgacacccctaca 780
QY 798 AGGCCATCCGGCTCATTTTGTATCATCGGGGTGTTTTTCATTTCTGACACCCCTACA 857
Db 781 atgtggctacccctctctctctctctctctctctctctctctctctctctctctctctct 840
QY 858 ATGTGGCTATCTCTCTCTCTCTATCAATCCATCTTATTTGGAATGACTGTGAGCGGA 917
Db 841 mgarsmwykkgacctgtgctgtgtgacagaggtgagctgagctgagctgagctgagctgag 900
QY 918 GCAAGCATCTGGACCTGGTCTGCTGTGACAGAGGTGATCGCTCTACTCCACTGTGCA 977
Db 901 tgaacccggtgactgacgcttgttggagagaggttcccgaaagtactcgcgcaacttst 960
QY 978 TGAACCCGGTGTACTAGCCCTTTGTTGGAGAGAGGTTCCGGAGTACTCTGCGCACCTCT 1037
Db 961 tccacagggcactgtgctgacactggcgagagatacatcccatctctctcttagtgagaagc 1020
QY 1038 TCCACAGGCACCTGCTCATGCACCTGGGCAGATACATCCCATCTCTTCTTCTAGTGAGAAGC 1097
Db 1021 tggaaagaacacgctgtctctcctccatccacagcagagcgaggaactctctatgtgttt 1080
QY 1098 TGGAAAGAACACGCTGTCTCTCCATCCACAGCAGAGCGGAACTCTCTATTGTGTTTT 1157
Db 1081 aggtagatgcagaaaattgcttaagaggaagacc 1116
QY 1158 AGGTAGATGCAGAAAATTGCTTAAGAGGAGGAGACC 1193

```

RESULT 3

ID T58783 standard; DNA; 1689 BP.

AC T58783;

DT 30-SEP-1997 (first entry)

DE Human C-C chemokine receptor 3 DNA.

KW Human; eotaxin; eosinophil; chemoattractant; stimulation;

KW accumulation; attraction; chemotaxis; diagnosis; prevention;

KW treatment; disease; inflammation; allergy; asthma; rhinitis;

KW hypersensitivity; lung; pneumonia; Loeffler's; syndrome;

KW interstitial; ILD; idiopathic pulmonary fibrosis;
KW rheumatoid arthritis; systemic; lupus erythematosus; SLE;
KW ankylosing spondylitis; scleritis; Sjogren's; polymyositis;
KW dermatomyositis; bowel; anaphylaxis; drug; penicillin;
KW cephalosporin; insect sting; Crohn's; ulcerative colitis;
KW spondyloarthritis; scleroderma; psoriasis; dermatitis;
KW dermatitis; eczema; atopic; urticaria; necrotizing; cutaneous;
KW vasculitis; myositis; fascitis; multiple sclerosis;
KW myasthenia gravis; juvenile onset diabetes; glomerulonephritis;
KW autoimmune; thyroiditis; Bechet's; graft; rejection;
KW transplantation; allograft; graft versus host; cancer;
KW leukocyte infiltration; reperfusion injury; atherosclerosis;
KW haematologic malignancy; septic; endotoxin; shock;
KW polymyositis; dermatomyositis; immunosuppression; immunodeficiency;
KW AIDS; radiation therapy; chemotherapy; autoimmune; corticosteroid;
KW C-C chemokine receptor 3; CRK3; ss.
FH Homo sapiens.
Key Location/Qualifiers
cds 181..1248
FT /*tag= a
FT /product= CRK3
PN WO9700960-A1.
PD 09-JAN-1997.
PR 21-JUN-1996; U10723.
PR 23-JUN-1995; US-494093.
PA (LEUK-) LEUKOSITE INC.
PI Mackay C, Newman W, Ponath PD, Qin S, Ringler DJ;
DR WPI: 97-087387/08.
DR P-PSDB; W10100.
PT New isolated human eotaxin gene - used to develop prods. for the
PT diagnosis and treatment of e.g. inflammation, allergies, auto-immune
PT disease, infections and tumours
PS Example 7; Page 97; 130pp; English.
CC The present sequence encodes human C-C chemokine receptor 3 (CRK3),
CC to which human eotaxin (hE), an eosinophil specific chemoattractant
CC capable of stimulating eosinophil accumulation and/or attracting
CC eosinophils (including chemotaxis), binds.
CC hE can be used to develop products for the diagnosis, prevention or
CC treatment of hE associated diseases or conditions. The products can
CC be used to treat inflammatory or allergic diseases and conditions,
CC including respiratory allergic diseases (e.g. asthma, allergic
CC rhinitis, hypersensitivity lung diseases or pneumonitis,
CC eosinophilic pneumonias such as Loeffler's syndrome and chronic
CC eosinophilic pneumonia, interstitial lung diseases (ILD) such as
CC idiopathic pulmonary fibrosis or ILD associated with rheumatoid
CC arthritis, systemic lupus erythematosus (SLE), ankylosing
CC spondylitis, systemic sclerosis, Sjogren's syndrome, polymyositis
CC or dermatomyositis), systemic anaphylaxis or hypersensitivity
CC responses, drug allergies (e.g. to penicillin and cephalosporins),
CC insect sting allergies, inflammatory bowel diseases (e.g. Crohn's
CC disease and ulcerative colitis), spondyloarthropathies,
CC scleroderma, psoriasis and inflammatory dermatoses (e.g.
CC dermatitis, eczema, atopic dermatitis, allergic contact dermatitis,
CC urticaria and necrotizing, cutaneous and hypersensitivity
CC vasculitis), eosinophilic myositis and fascitis, multiple
CC sclerosis, SLE, myasthenia gravis, juvenile onset diabetes,
CC glomerulonephritis, autoimmune thyroiditis, Bechet's disease, graft
CC rejection (e.g. in transplantation) including allograft rejection or
CC graft versus host disease and cancers with leukocyte infiltration
CC of the skin or organs. The products can also be used to treat other
CC diseases or conditions requiring the inhibition of undesirable
CC inflammatory responses, including reperfusion injury,
CC atherosclerosis, certain haematologic malignancies, cytokine
CC induced toxicity (e.g. septic or endotoxin shock), polymyositis,
CC dermatomyositis, immunosuppression (e.g. in individuals with
CC immunodeficiency syndromes such as AIDS, undergoing radiation
CC therapy, chemotherapy, therapy for autoimmune disease or other drug
CC therapy, such as corticosteroid therapy, which causes
CC immunosuppression), immunosuppression due to (e.g. congenital)
CC deficiency (e.g. in eotaxin) or infectious diseases such as parasitic
CC diseases.
CC Degenerate primers based on the guinea pig eotaxin amino acid
CC sequence were used for the reverse transcriptase polymerase chain

CC	reaction (RT-PCR) amplification of RNA isolated from inflamed, eosinophilic lung tissue obtained from Balb/c mice sensitised to CC ovalbumin. The amplification product was used as a probe to screen a human genomic library in vector EMBL3 SP6/T7 to obtain the hE gene.	Sequence	1689 BP;	431 A;	416 C;	344 G;	497 T;
	Query Match	93.2%;	Score 1112;	DB 32;	Length 1689;		
	Best Local Similarity	99.8%;	Pred. No. 0.00e+00;				
	Matches 1114;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps		
Db	167	caggggagaadtgaaatgacaacctcactagatacagttgagaccttgggtaccacatcct	226				
Qy	78	CAGGGAGAAGTGAATGACAACCTCACTAGATACAGTTGAGACCTTTGGTACCACATCCT	137				
Db	227	actataatgacgtggccctgctctgtaaaaagctgataccagagcactgatggcccaagt	286				
Qy	138	ACTATGATGACGTGGGCGCTGCTGTGAAAAAGCTGATACCAAGACATGATGGCCCAAGT	197				
Db	287	ttgtgccccgcgtgtactccctggtttccactgtggcctctcttgggcaatgtgggtgtgg	346				
Qy	198	TTGTGCCCGCGCTACTCCTCGTTCACGTGGGCGCTCTGGGCAATGTGGTGTGGTGG	257				
Db	347	tgatgtacctataaaataacagagaggtccgaaattatgaccaacatctacctgtctcaacc	406				
Qy	258	TGATGATCCTCATAAATACAGAGAGCTCCGAATATATGACCAACATCTACCTGCTCAACC	317				
Db	407	tggccatttgcgacctctctcctcgtcaccttccattcttgatccactatgtcgaagg	466				
Qy	318	TGGCCATTTCCGACCTGCTCTTCTCCTCGTCACCCCTCCATCTTGGATCCACTATGTACGGG	377				
Db	467	ggcataactgggtttttggccatggcatgtgtaagctctctcagggtttttatcacacag	526				
Qy	378	GGCATAACTGGGTTTTTGGCCATGGGCATGTGAAGCTCCTCTCAGGGTTTTATCACACAG	437				
Db	527	gcctgtacagcgagatcttttttcoataatcctgctgcacatcgacaggttacctggccattg	586				
Qy	438	GCCTGTGACAGCGAGATCTTTTTCATTAATCCTGCTGACAAATCGACAGGTACCTTGGCATTG	497				
Db	587	tccatctgtgtttgccccttcagcccgagcgtcacttttgggtctatccaccagcatcg	646				
Qy	498	TCCATGCTGTGTTTGCCCTTCGAGCCGGACGTGCTACTTTTGGTGTCAATCACCAACATCG	557				
Db	647	tcacctggggcctggcagtgctcagcagctcttctcgaatttatcttctatgagactgaag	706				
Qy	558	TCACCTGGGGCCCTGGCAGTGTGACAGCTCTTCCCTGAATTTATCTTCTATGAGACTGAAG	617				
Db	707	agtgtttgaagagactctttgcagtgctctttaaaccagaggatcacagtatatagctgga	766				
Qy	618	AGTGTGTTGAAGAGACTCTTTTGCAGTGCTCTTTATCCACAGAGGATACGATATATAGCTGGA	677				
Db	767	ggcatttccacactctgagaatgaccattctgtctcgttctcctcctcgtcgttatagg	826				
Qy	678	GGCATTTCCACACTGTGAGAATGACCATCTCTGTCTCGTTCCTCTCTGCTGCTGTTATGG	737				
Db	827	ccatctgtctacacaggaaatcaataaacgctgctgaggtgccccagtaaaaaaaagtaca	886				
Qy	738	CCATCTGCTACACAGGAATCATCAAAACGCTGCTGAGGTCGCCAGTAAAAAAGATACA	797				
Db	887	aggccatcogggtcatttttgttcacatgggggtgttttttcattttcttggcacaccctaca	946				
Qy	798	AGGCCATCCGGCTCATTTTGTTCATCATGGCGGTGTTTTTTCATTTTCTGGACACCTACA	857				
Db	947	atgtgactatcctctctctcctatcaatcacttatttggaaatgactgtgacgga	1006				
Qy	858	ATGTGGCTATCCCTTCTCTCTCTCTCAATCAATCATCTATTTTGGAAATGACTGTGACCGGA	917				
Db	1007	cgaagcatctggacctggctcatgctggttgacagaggtgatcgcttacttcccactgctga	1066				
Qy	918	GCAAGCATCTGGACCTGGTCATGCTGGTGACAGAGGTGATCGCCTACTCCCACTGCTGCA	977				
Db	1067	tgaacccggtgatactacgaccttttgttggagagaggttccgggaagtaccttggccacttct	1126				

Qy	978	TGAACCGGCTGATCTACTAGCGCTTTGTGGAGAGAGAGGTTCGGAAAGTACCTCTCGCGCCACTTCT	103			
Db	1127	tccacaggcacttgcctcatgcacctggcagacatcacatcccattcctcttagtgagaagc	1186			
Qy	1038	TCCACAGGCACTTTCCTCATGCACCTTGGCGAGATACATCCCATTCTCTCTAGTGAGAAGC	1097			
Db	1187	tggaagaagaacagctctgtctctccatccacagcagagccggaactctctattgtgttt	1246			
Qy	1098	TGGAAGAACCACTGCTGCTCTCCATCCACAGCAGACCGGAACCTCTATTGTGTTTT	1157			
Db	1247	aggtagatgcagaaaattgcctaaagaggaagacc	1282			
Qy	1158	AGGTAGATGCAGAAAATTGCCTAAAGAGGAGGACC	1193			
RESULT 4						
ID	T31334 standard; DNA; 1689 BP.					
AC	T31334;					
DT	15-NOV-1996 (first entry)					
DE	CC-chemokine receptor 3 genomic DNA.					
KW	CC-chemokine receptor 3; CRP-3; Eos-L2; inhibitor; antisense;					
KW	antiinflammatory; eosinophil; ds.					
OS	Homo sapiens.					
FH						
FT	Location/Qualifiers					
FT	cds					
FT	181..1248					
FT	/*tag= a					
FT	1007..1008					
FT	/*tag= b					
FT	/*note= "CKR-3 genomic clone has CG at positions					
FT	1007-1008, coding for threonine (ACG) at					
FT	position 276; a cDNA clone has GC at					
FT	these positions, coding for serine (AGC)"					
FT	misc_difference 1291					
FT	/*tag= c					
FT	/*note= "base n at position 1291 is not identified					
FT	in the specification"					
FT						
PN	W09622371-A2.					
PD	25-JUL-1996.					
PF	19-JAN-1996; U00608.					
PR	19-JAN-1995; U5-375199.					
PA	(BGHM) BRIGHAM & WOMENS HOSPITAL.					
PA	(CHIL-) CHILDRENS MEDICAL CENT.					
PA	(LEUK-) LEUKOSITE INC.					
PI	Gerard CJ, Gerard NP, Mackay CR, Ponath PD, Post TW;					
PI	Qin S;					
DR	WFI; 96-354528/35.					
DR	P-PSDB; W03376.					
PT	Mammalian chemokine receptor-3 and related nucleic acids - useful to					
PT	identify receptor inhibitors to treat inflammatory disease, e.g.					
PT	autoimmune disorders, certain cancers, etc.					
PS	Claim 1: Page 109; 153pp; English.					
CC	A genomic DNA clone (T31334) codes for a novel receptor (W03376),					
CC	designated Eos L2 or C-C chemokine receptor 3 (CCR-3), involved					
CC	in leukocyte migration associated with inflammation. It was					
CC	isolated from a human genomic library in EMBL3 SP7/77 vector by					
CC	screening with a PCR fragment generated from eosinophil cDNA					
CC	using degenerate primers (see also T31337-44). A CCR-3 cDNA					
CC	clone (T31335) was also isolated, and a consensus sequence is					
CC	given in T31336. The genomic and cDNA clones can be used for					
CC	the prodn. of recombinant CCR-3 in host cells, or to design					
CC	antisense sequences useful for treating inflammatory disease.					
SO	Sequence 1689 BP; 431 A; 416 C; 344 G; 497 T;					
Query Match 93.2%; Score 1112; DB 23; Length 1689;						
Best Local Similarity 99.8%; Pred. No. 0.00e+00;						
Matches 1114; Conservative 0; Mismatches 2; Indels 0; Gaps						
Db	167	cagggagaagtgaatgacaacctcactagatagacttgagacaccttgggtaccacatcct	226			
Qy	78	CAGGGAGAGTGAATGACAACTCAGTAGATACAGTTGAGACCTTTGGTACCAATCCT	137			
Db	227	actatgatgacgtgggcctgctgtgaaaaagctgacaccagagcactgatggccagct	286			

QY 138 ACTATGATGACGTGGCCCTGCTCTGTGAAAAAGCTGATACAGAGCAGCTGATGGCCCACT 197
Db 287 ttgtgccccctgtactccctggttttccactgtgagccctcttggaacatgtggtgtg 346
QY 198 TTGTGCCCCCGCTGTACTCCCTGGTGTTCACCTGGGCCCTCTTGGGCAATGTGGTGTG 257
Db 347 tgatgatcctcataaaataacagaggtccgaattatgaccaaactctacctgtcctaacc 406
QY 258 TGATGATCCTCATAAAATACAGAGGCTCCGAATTATGACCAACATCTACCTGCTCAACC 317
Db 407 tggccatttcggacctgtcttctctcgtcgaacctccattcttgatccactatgtcaggg 466
QY 318 TGGCCATTTTCGACCTGCTCTTCTCTGTCACCTTCCATTTCTGGATCCACTATGTGAGGG 377
Db 467 ggcataactgggtttttggccatggcatgtgtaagctctctcagggtttttatcacacag 526
QY 378 GGCATAACTGGGTTTTTGGCCATGGCATGTGTAAAGCTCTCTCAGGGTTTTTATCACACAG 437
Db 527 gctgttacagcagagatctttttcataatcctcgtcgtgacaatcgacaggtacctggccattg 586
QY 438 GCTGTGACAGGAGATCTTTTTCATATCTCTGCTGACATCGACAGGTACCTGGCCATTG 497
Db 587 tccatcgtgtgtttgcccctcgagccggactgtcacttttgggtgtcactcaccagcatcg 646
QY 498 TCCATGCTGTGTTTGGCCCTTCGAGCCGGACTGCTCACTTTTGGTGTATCATCACCAGCATCG 557
Db 647 tcaactggggcctggcagtgctagcagctcttctcgaattatctctatgagactgaag 706
QY 558 TCACCTTGGGGCCTGGAGTGTGCTAGCAGCTCTTCTGAAATTAATCTTATGAGACTGAAG 617
Db 707 agtgtttgaagagactctttcagtgctctttaccagaaggtacagatatagctgga 766
QY 618 AGTGTGTTGAAGAGACTCTTTGACGTGCTCTTACCAGAGGATACATATAGCTGGA 677
Db 767 ggcatttcacacactctgagaatgacctctctgtctcgtctcctcctcgtcgttatgg 826
QY 678 GGCATTTCCACACTCTGAGAATGACCATCTTCTGCTGTTCTCCCTCTGCTGTTATGG 737
Db 827 ccaatcgtctacacaggaatcaataaacgctgctgaggtgcccagtaaaaaaagtaca 886
QY 738 CCATCTGCTACACAGGAATCATCAAAACGCTGCTGAGGTGCCCCAGTAAAAAAAGTACA 797
Db 887 aggcacatcgggtcatttttctcatcatgctgctgtgttttctcttcttgacacccctaca 946
QY 798 AGCCCATCCGGCTCATTTTGTGTCATGTCGCGGTGTTTTTCATTTTCTGGACACCTTACA 857
Db 947 atgtggctatcctctctctctcctatacaatccatcttatttggaaatgactgtgagcgga 1006
QY 858 ATGTGGCTATCCTTCTCTCTCTCTATCAATCCATCTTATTTGGAATGACTGTGAGCGGA 917
Db 1007 cgaagcatctggacctgggtgctgctggtgacagaggtgctgctcactcctcactgtgca 1066
QY 918 GCAAGCATCTGGACCTGGTCTGCTGCTGACAGAGGTGATCGCTACTTCCACTGCTGCA 977
Db 1067 tgaacccggtgatctacgcttttggtagagaggttccggaagtagtacctcgcacctttct 1126
QY 978 TGAACCCGGTGATCTACGGCTTTTGTGGAGAGAGGTTCGGGAAGTACCTCGCCCACTTCT 1037
Db 1127 tccacagggcacttgctcatgcactcctgggcagatacatccctctcctcctagtgagaagc 1186
QY 1038 TCCACAGGCACCTTGTCTATGCACTGGGACAGATACATCCCATTTCTTCCATGTGAGAACG 1097
Db 1187 tggaaagaacacagctctgtctctccatccacagcagagcgggaactctctattgtgtttt 1246
QY 1098 TGGAAAGAACCACTGCTGCTCTCTCCATCCACAGCAGAGCCGGAACCTCTCTATTGTGTTT 1157
Db 1247 aggtagatgcagaaaattgctctaaagaagagacc 1282
QY 1158 AGGTAGATGCAGAAAATTGCTTAAGAGGAAGGACC 1193

RESULT 5

ID T85162 standard; cDNA; 1915 BP.

AC T85162; AC
DT 14-DEC-1997 (first entry)
DE Human chemokine receptor 88-2B cDNA.
KW Chemokine receptor 88-2B; atherosclerosis; rheumatoid arthritis;
tumour; asthma; viral infection; AIDS; inflammation;
KW autoimmune disease; therapy; diagnosis; leukocyte trafficking;
KW G protein coupled receptor; human; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 362..1429 /*tag= a

PN W09722698-A2.
PD 26-JUN-1997.
PF 20-DEC-1996; U20759.
PR 07-JUN-1996; US-661393.
PR 20-DEC-1995; US-575967.
PA (ICOS-) ICOS CORP.
PI Gray PW, Raport CJ, Schweickart VL;
DR WPI; 97-341689/31.
DR P-PSDB; W27124.
PT New nucleic acid encoding chemokine receptors 88-2B and 88C - used
to modulate leukocyte trafficking, e.g. for treatment of
PT inflammation, tumours, viral infections, autoimmune diseases, etc.
PS Claim 7; Page 48-50; 65pp; English.
CC This sequence comprises a full-length cDNA coding for novel human
chemokine receptor 88-2B (W27124), a G protein coupled receptor that
is involved in leukocyte trafficking. The 88-2B cDNA was obtained
from a macrophage cDNA library using 88-2B-specific primers. A
CC full-length clone (see T89161) for chemokine receptor 88C (W27123)
was also obtained. 88C and 88-2B cDNAs can be used to produce
CC recombinant polypeptides in transformed host cells for use in the
treatment of e.g. atherosclerosis, rheumatoid arthritis, tumours,
CC asthma, viral infection, AIDS and inflammatory conditions. Nucleic
CC acid fragments can be used to isolate genomic sequences, to detect
alleles of the gene (for diagnosis or in gene therapy), to alter
CC receptor genetics to facilitate identification of modulators and to
CC produce knockout animals, and (antisense forms) to alter/study the
CC genetics and expression of the receptor.
SQ Sequence 1915 BP; 488 A; 470 C; 373 G; 584 T;

Query Match 93.0%; Score 1110; DB 34; Length 1915;
Best Local Similarity 99.9%; Pred. No. 0.00e+00;
Matches 1116; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 348 caggggagagtgaaatgacaaactcactcagatagatagacactttgttaccacatcct 407
QY 78 CAGGGAGAGTGAATGACAACTCCTACTAGATACAGCTTGAGACCTTTGGTACCACATCCT 137
Db 408 actatgatcacgtggcgctgctctgtgaaaagctgataccagagcactgatggccag 467
QY 138 ACTATGATGACGTGGGCCCTGCTCTGTGAAAAAGCTGATACAGAGCAGTGTATGGCCCACT 197
Db 468 ttgtgccccctgtactccctcgtgttccactgtggccctcttgggcaatgtggtgtg 527
QY 198 TTGTGCCCCCGCTGTACTCCCTGGTGTTCACGTGTGGCCCTCTTGGGCAATGTGGTGTG 257
Db 528 tgatgatcctcataaaataacagaggtccgaattatgaccaaactctacctgtcctaacc 587
QY 258 TGATGATCCTCATAAAATACAGAGGCTCCGAATTATGACCAACATCTACCTGCTCAACC 317
Db 588 tggccatttcggacctgtcttctcgtcgaacctccattcttgatccactatgtcaggg 647
QY 318 TGGCCATTTTCGACCTGCTCTTCTCTGTCACCTTCCATTTCTGGATCCACTATGTGAGGG 377
Db 648 ggcataactgggtttttggccatggcatgtgtaagctctcctcagggtttttatcacacag 707
QY 378 GGCATAACTGGGTTTTTGGCCATGGCATGTGTAAAGCTCTCTCAGGGTTTTTATCACACAG 437
Db 708 gctgttacagcagagatctttttcataatcctcgtcgtgacaatcgacaggtacactgtgcccattg 767
QY 438 GCTGTGACAGGAGATCTTTTTCATATCTCTGCTGACAAATCGACAGGTACCTGCGCCATTG 497
Db 768 tccatcgtgtgttggccctcgagcccgagctgtcacttttgggtgtcactcaccagcagctg 827

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|||||
498 TCCATGCTGTGTTGCCCTTCGAGCCCGACTGTCACATTTTGGTGTCTATCACCAGCATCG 557
Db      tcaactggggcctggcagctagcagctctctcctgaatttatcttatgagactgaag 887
558 TCACCTGGGGCTGGCAGCTGTAGCAGCTCTTCCTGAATTTATCTTCTATGAGACTGAAG 617
Db      agtgtttgaagagacttttgagctgctctttaccacagagatacagtatatagctgga 947
618 AGTTGTTTGAAGAGACTCTTTGCACTGCTCTTTACCCAGAGGATACAGTATATAGCTGGA 677
Db      ggcatttcacactctgagaatgaccattctctgctctgctctcctctgctgtatgg 1007
678 GGCATTTCACACTGAGATGACCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 737
Db      ccattctcacacaggaatcatcaaacgctgctgagtgccccagtaaaaaaagtaca 1067
738 CCATCTGTACACAGGAATCATCAAAACGCTGCTGAGTGCCCCAGTAAAAAAGTACA 797
Db      aggcacatcggtcatttttgcatactgagcggtgtttttcattttctggcacacctaca 1127
798 AGGCCATCCGGCTCATTTTCTCATCATGCGCGGTGTTTTTCATTTCTGGACACCCCTACA 857
1128 atgtggctatcctctctctcctcatcaatccatcttatcttggaatgactgtgagcga 1187
858 ATGTGGCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 917
Db      gcaagcatctggacctgctatgctgctggtagacagagtgatgcgctactccccactgctgca 1247
918 GCAAGCATCTGACCTGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCA 977
Db      tgaacccggtaatacagcctttgttgagagaggttcgcggaagtacacctgcgccacttct 1307
978 TGAACCCGGTATCTACGCCCTTTCTTGAGAGAGAGTTCCGGAAGTACCTGCGCCACTTCT 1037
Db      tccacagcacttctcatgacacatggcagacatcacatccattctctctagtgaagc 1367
1038 TCCACAGCACTTCTCTATGACCTGGCAGATATATCCCAATCTCTTCTAGTGAGAAGC 1097
Db      tggaaagacacagctctgtctctccatccacagcagagccggaaactctctattgtttt 1427
1098 TGAAGAAGAACAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTTT 1157
Db      aggtcagatgcagaaaattgctctaaagaggaagacc 1464
1158 AGGT-AGATGCAGAAAATTGCTTAAGAGGAAGGACC 1193
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RESULT 6
ID T93601 standard; cDNA; 5099 BP.

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T93601;
07-MAY-1998 (first entry)
DE Human eosinophil eotaxin receptor CC CKR3 encoding cDNA.
KW Eosinophil eotaxin receptor; CC CKR3; human; treatment; dermatitis;
KW atopic condition; allergic rhinitis; conjunctivitis; bronchial asthma;
KW beta-chemokine receptor; viral infection; ss.
OS Homo sapiens.
FH Key
FT misc_feature 1..3586
FT note= "5' genomic DNA flanking sequence"
FT note= "3587..4654"
FT note= "/*tag= b"
FT note= "/*product= "human eosinophil eotaxin receptor"
FT misc_feature 4655..5099
FT note= "/*tag= c"
FT note= "terminator region"
FN WO9741154-A1.
PD 06-NOV-1997.
PF 24-APR-1997; U06568.
PR 17-JAN-1997; GB-000894.
PR 26-APR-1996; US-016158.
PR 26-APR-1996; US-017113.
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(MERI ) MERCK & CO INC.
PI Daugherty BL, Demartino JA, Siciliano SJ, Springer MS;
DR WPI; 97-549685/50.
DR P-PSDB; W31850.
PT New isolated human eosinophil eotaxin receptor - used to develop
PT products for treating and preventing atopic conditions e.g. allergic
PT rhinitis, dermatitis, conjunctivitis and bronchial asthma
PS Claims 12, 13, 14; Pages 16-20; 51pp; English.
CC This cDNA encodes a human eosinophil eotaxin receptor, flanked by a 5',
CC 355 amino acid eosinophil eotaxin receptor protein, flanked by a 5',
CC genomic DNA sequence and a 3' terminator region. This novel eosinophil
CC eotaxin receptor is a human beta-chemokine receptor designated CC CKR3.
CC Agents which bind to this eosinophil eotaxin receptor can be used for
CC the treatment and prevention of atopic conditions such as allergic
CC rhinitis, dermatitis, conjunctivitis and bronchial asthma. Agents which
CC block this eosinophil eotaxin receptor can be used to prevent viral
CC infection in healthy individuals and slow or halt viral progression
CC in infected patients.
SQ Sequence 5099 BP; 1388 A; 1171 C; 1013 G; 1527 T;
Query Match 93.0%; Score 1110; DB 38; Length 5099;
Best Local Similarity 99.9%; Pred. No. 0.00e+00;
Matches 1116; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Db 3573 cagggagaagtgaatgacaacctcactagatcacagttgagacctttgggtaccacatcct 3632
QY 78 CAGGGAGAAGTGAATGACAACCTCAGTAGATACAGTTGAGACCTTTGGTACCACATCCT 137
Db 3633 actatgatgacgtgggctgctctgtgaaaaagctgtaccagagacctgaggtcccaagt 3692
QY 138 ACTATGATGACGTGGGCTGCTCTGTGAAAAGCTGTATACCAGAGCACTGATGCCAGT 197
Db 3693 ttgtgccccgcgtactcctctgttccactgtggcctctgtggcaatgtgtgtgg 3752
QY 198 TTGTGCCCCCGCTGCTACTCCCTGGTGTCTACTGTGGGCCCTCTTGGGCAATGTGTGTGG 257
Db 3753 tgatgatctctcaataatacagagggtccgaattatgacaaacatctacctgctcaacc 3812
QY 258 TGATGATCTCTATAAATACAGGAGGCTCGAATATATGACCAACATATACCTGCTCAACC 317
Db 3813 tggccatttcggacctctctctctctctctctctctctctctctctctctctctctctctct 3872
QY 318 TGGCCATTTCCGACCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 377
Db 3873 ggcataactgggttttggccatggcagctgtgaagctcctctcaggggttttatcacacag 3932
QY 378 GGCATAACTGGGTTTTTGGCCATGGCATGTGTAAAGCTCTCTCAGGGTTTTATCACACAG 437
Db 3933 gcttgtacagcagatcttttttataatcctgtgacaatcgacaggtacctggccattg 3992
QY 438 GCTTGTACAGCGAGATCTTTTTCATATCTGCTGTGACAAATCGACAGGTACTGTGCCATTG 497
Db 3993 tcaatgtgtgttggcctctggagcccgacctgtcaattttgtgtgtctatcacacagatcg 4052
QY 498 TCCAATGCTGTGTGTGGCCCTTCGAGCCCGGACTGTCACTTTTGTGTCTATCACCAGCATCG 557
Db 4053 tcacctgggcccctggcagtgctagcagctctctctgaatttatctctatgagactgaag 4112
QY 558 TCACCTGGGCGCTGGCAGTCTGTAGCAGCTCTTCTGAAATTTATCTTATGAGACTGAAG 617
Db 4113 agttgtttgaagagactcttttgagctgctctttaccacagaggaacacagtatatagctgga 4172
QY 618 AGTTGTTTGAAGAGACTCTTTGACAGTCTCTTTACCCAGAGGATACAGTATATAGCTGGA 677
Db 4173 ggcatttcacactctgagaatgacacatctctctgtctctgtctctctctctctctctct 4232
QY 678 GGCATTTCCACACTCTGAGAATGACCATCTTCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 737
Db 4233 ccactctcacacaggaatcatcaaacgctgctgaggtgccccagtaaaaaaagtaca 4292
QY 738 CCATCTGCTACACAGGAATCATCAAAACGCTGCTGAGGTGCCCGAGTAAAAAAGTACA 797
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Db	599	gaaatccaaagctgtccggttgatttggattttgtcatcatcatgatactctttttctctctttggac	758
Qy	790	AAAGTACAAGGCCATCCGGCTCAATTTTTGTCAATCATGCGGGTGTATTTTTCAATTTCTGGAC	849
Db	759	ccctacaatttgactatactattctctgtttttccaagactctctgttccacccatgagtg	818
Qy	850	ACCTACAAATGTGGCTATCTCTCTCTCTCCATCAATCCATCTTATTTGGAAATGACTGTG	909
Db	819	tgagcagagcagacatttgaccctggctgtgcaagtgcgaggagtgatcgccctacacgca	878
Qy	910	TGAGCGGAGCAAGCATCTGGACCTGGTCAATGCTGGTGACAGAGGTGATCGCTACTCCCA	969
Db	879	ctgtgtgttcaacccagtgatctacgccttctgtgtgtgagagttccggaagtacctcg	938
Qy	970	CTGTGTCATGAACCCGGTGATCTACGCTTTGTGTGGAGAGAGTTCCGGAAGTACCTGGG	1021
Db	939	gcagtgtttccacagggtgtgctgtgcacctgggttaattggctccctctccctccct	998
Qy	1030	CCACTCTTCCACAGGCACCTGTGTCATGCACCTGGGAGATACATCCCATTCCTTCCTTAG	1088
Db	999	ggacaggctggagaggttcagctccacatctcctccacaggggagatgaactctctgc	1059
Qy	1090	TGAGAAGCTGGAAAGACCAAGCTCTGCTCTCCATCCACAGCAGACCGGAAGTCTCTAT	1144
Db	1059	tggggtt	1064
Qy	1150	TGTGTT	1155

RESULT	9	
ID	Q62695	standard; DNA; 1495 BP.
AC	Q62695;	
DT	30-JAN-1995	(first entry)
DE	C-C chemokine receptor DNA.	
KW	C-C CKR-1; cytokine; inflammation; ds.	
OS	Homo sapiens.	
PN	W09411504-A.	
PD	26-MAY-1994.	
FF	04-NOV-1993;	U10672.
PR	10-NOV-1992;	US-974025.
PA	(GETH) GENENTECH INC.	
PI	Horuk R, Neote K, Schall T;	
DR	WPI: 94-183505/22.	
DR	P-PSDB: R52749.	
PT	New C-C chemokine receptor and nucleic acid -	are used to develop
PT	prods. for use in diagnosis and therapy of inflammation and other	
PT	cytokine-mediated disorders	
FS	Claim 17; Fig 9; 90pp; English.	
CC	The sequence is that of the C-C chemokine receptor gene which was	
CC	isolated by PCR from PMA treated HU60 cells using PCR primers whose	
CC	sequence was designed to correspond to conserved sequences in two	
CC	transmembrane regions of known cytokine receptors. The sequence can	
CC	be used in therapeutic or diagnostic compns. for inflammation and	
CC	other cytokine mediated disorders.	
SQ	Sequence 1495 BP; 348 A; 389 C; 361 G; 397 T;	
Query Match	35.94;	Score 428; DB 11; Length 1495;
Best Local Similarity	72.24;	Pred. No. 1.28e-295;
Matches	697; Conservative	0; Mismatches 269; Indels 0; Gaps
Db	99	ggcccaactgctgccccctctgtactccttgggtatttgcattggcctcgtgtggaacat 158
Qy	190	ggccacagtttgccccccggtgtactcccggtgttacctgtgggctcttgggcaatgt 249
Db	159	ctcgtggtcctggtccttgtgcaatacagaagcgtctcaaaaaacatgaccagcatctacct 218
Qy	250	ggcgtggtgatgcctctcatalaaatcacagagcctccgaattatgaccaaacatctacct 309
Db	219	octgaacctggccaattctctgacctgctctccctgtgtcaacgctccctctctggtacgacta 278
Qy	310	gctcaactggcccaatttcggacctgcgtcttcctcgtcatcccttcccatctfgggatccacta 369
Db	279	caagtgaagatgactcgggttttttggtgatgcgcattgtaaagatcctctcctgggtttta 338

QY 370 TGTGAGGGGATCACTGGGTTTTGGCCATGCTGTAAGCTCTCTCAGGGTTTTA 429
Db 339 ttacacagcgtgttacacagagatctttttatcatcctctgctgagcattgacaggtacct 398
QY 430 TCACACAGCCTTGTACAGGGAGATCTTTTCAATATCCCTGCTGACATCGACAGGTACCT 489
Db 399 ggcacatgctccacgcgctgttgccctgcggcagcagcgtcaccttttgggtgctacac 458
QY 490 GGCATGTTCATGCTGTGTGGCTTCGAGCCGGATGTCATCTTTGGTGTGATCAC 549
Db 459 cagcatcatcatttggccctggccatcttggcttcacagcaggttttcttccaa 518
QY 550 CAGCATGCTGCTGAGGCTGAGCAGTCTTCTGATTTATCTTCTATGA 609
Db 519 gaccacaatgggaattcaactcaccacacacctgcagccttctctcaccagaagcctacg 578
QY 610 GACTGAAGAGTGTGTGAAGAGACTCTTTGCAGTGTCTTTACCCAGAGGATACAGTATA 669
Db 579 agagtggagcgtgttcagcgtctgaacctgaacctcttggcgtggtattcccttgg 638
QY 670 TAGCTGGAGGCATTTCCACACTGTGAATGACCATCTTCTGCTGCTCTCCCTCTGCT 729
Db 639 ggtcatgattcatctgtacacagggattataaagattctgtaagcagcaccacaaatgagaa 698
QY 730 CGTTATGGCCATCTGCTACACAGGAATCATCAAAAGCTGCTGAGGTGCCCGACATAAAA 789
Db 699 gaaatccaaagctgctgttgaatttttgaatcgtatcattttttttttttttttggac 758
QY 790 AAAGTACAAGGGCATCCGGCTCATTTTGTCTATCATGCGGGTGTCTTTCATTTCTGGAC 849
Db 759 cccctacaatttgactatactattctgttttccaaagcttcctgttccaccatgagt 818
QY 850 ACCCTACAATGTGGCTATCT 909
Db 819 tgagcagagcagcatttgacccgtgctgtgcaagtgacggaggtgacgctacacgca 878
QY 910 TGAGCGGAGCAAGCATCTGAGCTGTGATGCTGTGTGACAGAGGTGATCGCCTACTCCA 969
Db 879 ctgctgttccaaacccagtgatcagcctctgtgtgtgagaggttcgggaagctcctgcg 938
QY 970 CTGCTGCATGAACCCGGTATCTACGCCCTTGTGGAGAGAGGTTCCGGAAGTACCTGGC 1029
Db 939 gcagttgttccacagcgtgtggtgtgacctgtgttaaatggctcccttctctcct 998
QY 1030 CCACCTTCTTCCAGAGCATCTGCTATGACCTTGGGAGATACATCCCATCTCTCTCTAG 1089
Db 999 ggcagcgtggagaggttcagctccacatctccctccacaggggagcagcagcctctgc 1058
QY 1090 TGAGAGCTGGGAAGAACACAGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1149
Db 1059 tggggtt 1064
QY 1150 TGTGTT 1155

RESULT 10
ID T90384 standard; DNA; 2156 BP.
AC T90384;
DE Human MIP-1 alpha (first entry)
DE Human MIP-1 alpha/RANTES receptor gene.
KW Macrophage inflammatory protein-1 alpha; MIP-1 alpha;
KW reduced upon activation normal T expressed and secreted; RANTES;
KW receptor; cytokine; antiinflammatory; inflammation; human; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 63..1130
FT /*tag= a
PN US5652133-A.
PD 29-JUL-1997.
PF 28-JAN-1993; 012988.
PR 28-JAN-1993; US-012988.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Murphy PM;
DR WPI: 97-392945/36.
DR P-PSDB: W26588.
PT MIP-1-alpha and RANTES receptor nucleic acid - used to develop
PT products for the detection of these cytokine(s) and their receptors,
PT particularly in inflammatory processes
PS Claim 1: Column 11-16; 12pp; English.
CC This nucleic acid sequence encodes a claimed receptor for macrophage
CC inflammatory protein-1 alpha (MIP-1 alpha) and regulated upon
CC activation normal T expressed and secreted (RANTES) protein. Also
CC claimed are: (1) a subsequence of the nucleic acid, having at least
CC 12 contiguous nucleotides; (2) a cell transformed or transfected
CC with the nucleic acid; and (3) a purified MIP-1 alpha/RANTES receptor
CC polypeptide. The products can be used for detecting the MIP-1
CC alpha/RANTES receptor and polymorphisms in physiological samples.
CC In addition, the receptor can be expressed and used to assay for
CC MIP-1a/RANTES in biological samples. The quantitation of MIP-1
CC alpha/RANTES is useful for monitoring the levels of these cytokines
CC in a patient. Such measurements are useful in following the anti-
CC inflammatory effects of drugs and prospective usefulness of new anti-
CC inflammatory agents.
SQ Sequence 2156 BP; 538 A; 547 C; 504 G; 567 T;

Query Match 35.9%; Score 428; DB 34; Length 2156;
Best Local Similarity 72.2%; Pred. No. 1.28e-295;
Matches 697; Conservative 0; Mismatches 269; Indels 0; Gaps 0;
Db 161 ggcacacatgtgccccctctgtactccttggatttctgcttgcctggctgggaaacat 220
QY 190 GGGCCAGTTGTGCCCCGCTGTACTCCCTGGTGTACTGTGGCCCTCTTGGGCAATGT 249
Db 221 cctgtgtctcctgtgcttctgcaatacaagaggctaaacacatgaccagcatcact 280
QY 250 GGTGTGTGTGATGATCTCTATAAAATACAGGAGGCTCCGAATATGACCAACATCTACT 309
Db 281 cctgaacctggccattctgacctctctctctgtctacgcttccctctctgtgacgcta 340
QY 310 GCTCAACCTGGCCATTTGGGACCTGCTCTTCTCTGCTACCTCTCCATTTCTGGATCACTA 369
Db 341 caagttgaagtgactgggttttgggtgatgccatgtgtaagatcctctctctgggttta 400
QY 370 TGTACAGGGGGCATAACTGGGTTTTTGGCCATGGCATGTGTAAAGCTCCTCTCAGGGTTTTA 429
Db 401 ttacacagcgtgttacacagcagatctttttatcatcctgtgctgacgattgacaggtacct 460
QY 430 TCACACAGCCTTGTACAGCGAGATCTTTTTCATAATCTGCTGACAATCGACAGGTACCT 489
Db 461 ggcacatgctccacgcgctgttgccttgcggcagcagcctcacttttgggtgctacac 520
QY 490 GGCATGTGCCATGTGTGTGGCTTTCGAGCCGGAGTGTACCTTTTGGTGTCTATCAC 549
Db 521 cagcatcatcatttggccctggccatcttggcttccatgccagcgttatacttttccaa 580
QY 550 CAGCATGCTGCTACCTGGGCTGGCAGTGTAGCAGCTCTTCTCTGAATTTATCTTCTATGA 609
Db 581 gaccacaatgggaattcaactcaccacacacctgcagccttctctcaccagaagcctacg 640
QY 610 GACTGAAGAGTGTGTGAAGAGACTCTTTGACGTGCTCTTTACCCAGAGGATACAGTATA 669
Db 641 agagtggagcgtgttccagcctctgaaactgaaccttttggcgtggtattgcctttgt 700
QY 670 TAGCTGGAGGCATTTCCACACTCTGAGAAATGACCATCTTCTGCTGCTCTCTCTCTCTCT 729
Db 701 ggtcatgattcatctgtcacacagggattataaagattctgttaagcagcaccacaaatgagaa 760
QY 730 CGTTATGGCCATCTGCTACACAGGAATCATCAAAAGCTGCTGAGGTGCCCGACGTAAAAA 789
Db 761 gaaatccaaagctgtccogtttggatttttgcatacatcatcttttttctctttggac 820
QY 790 AAAGTACAAGGGCATCCGGCTCATTTTGTCTATCATGCGGGTGTCTTTCATTTCTGGAC 849
Db 821 cccctacaatttgactatactattctgttttccaaagacttcctgttccaccatgagt 880

CC using primers (see T85176-77) based on human 88C cDNA (see T85161).
CC The macaque 88C nucleotide sequence is 98% identical to that of
CC human 88C. 88C cDNAs can be used to produce recombinant
CC polypeptides in transformed host cells for use in the treatment of
CC e.g. atherosclerosis, rheumatoid arthritis, tumours, asthma, viral
CC infection, AIDS and inflammatory conditions. Nucleic acid
CC fragments can be used to isolate genomic sequences, to detect
CC alleles of the gene (for diagnosis or in gene therapy), to alter
CC receptor genetics to facilitate identification of modulators and to
CC produce knockout animals, and (antisense forms) to alter/study the
CC genetics and expression of the receptor.
SQ Sequence 1059 BP; 249 A; 274 C; 227 G; 309 T;

Query Match 18.7%; Score 223; DB 34; Length 1059;
Best Local Similarity 66.0%; Pred. No. 8.30e-141;
Matches 563; Conservative 0; Mismatches 280; Indels 10; Gaps 9;
98 tgcctccgctctactcaactggtgttcattcttgggtttgtgggcaacatactggtcgtcc 157
Qy 201 TGGCCCCGCTGTACTCCCTGGTGTTCACCTGTGGGCTCTTGGGCAATGTGGTGGTGA 260
Db 158 tcaactgataaactgcaaaaggctgaaagcatgactgacatctactctgctcaactcgg 217
Qy 261 TGATCCTCATAAATACAGAGGCTCCGAATATGACCAACATCTACCTGTCTCAACCTGG 320
Db 218 caactctgactgtttcttcttactgtctccctcttgggtcactatg-ctgctgcc 276
Qy 321 CCAATTTCGAGCTGCTTCCCTCGTCACCTTCCATTTCGATTCACATCTGTCAGGGGGC 380
Db 277 c--agtgagacttggaaatacaatgtgcaactcttgacagggctctattttatagct 334
Qy 381 ATAAGTGGGTTTGGCCATGCGCATGTGTAAGCTCTCTCAGGGTTTATACACAGGCT 440
Db 335 tctctctggaattcttctcatctctcctgacaaatcgatgactgtagtctggtctatcgtcc 394
Qy 441 TGTACAGCGAGATCTTTTTCATAATCCTGCTGACAATCGACAGGTACCTGGCCATGTCC 500
Db 395 atgctgtgttctttaaagccaggaacagtcactcttgggggtgacagtgatga 454
Qy 501 ATGCTGTGTTGCCCTTCGAGCCGGATGTCTACATTTGGTGTATCATCCAGACATCGTGA 560
Db 455 ctgggtggtggtgctgtgttctctctccaggaatcatctttaccagatctcagag 514
Qy 561 CTGGGGCTGGCATGTGATGAGCTCTCTCTGATTTATCTTCTATGAGACTGA-AGAG 619
515 aagttcttcattacacct-gcagctctcatcttccatcacagt-cagtatcaattctgaa 572
Qy 620 TTGTTTGAAGAGACTCTTTGCAGTGTCTTTTACCAGAGGATACAGTATATAG-CTGGAG 678
Db 573 gaatttccagacattaaagatggttcattcttgggggtggtcctgcgctgctgtcatggt 632
Qy 679 GCATTTCCACACTCTGAGAATGACCATCTTCTGCTCTGCTCTCCCTCTGCTGTATGGC 738
Db 633 catctgctactcggaaactcctgaaactctgctcgggtgtgcaaacgagaagaagaca 692
Qy 739 CATCTGCTACAGAGAAATCATCAAAACGGCTGCTGAGGTGCCCCAGTAAAAA-AA-AGT-A 795
Db 693 cagggtggtgagcttatcttcaccatcatgattgtttattttctcttggggctcccta 752
Qy 796 CAAGGCCATCCGGCTCATTTTGTTCATCATGCGGCTGTTTTTCATTTCTGGACACCCTA 855
Db 753 caacattgtctctctcgaacaccttcacgaagtattcttggcctggaataatgcaatag 812
Qy 856 CAATGTGGCTATCTCTCTCTCTATCAATCCATCTTATTTGGAAATGACTGTGAGCG 915
Db 813 ctctaacaggttggacaaagccatcagggtgacagactcttggatgacacactggtg 872
Qy 916 GAGCAAGCATCTGGACCTTGGTTCATGCTGGTGACAGAGGTGATCGGCTACTCCCACTGCTG 975
Db 873 catcaacccccatcatctatgctcttgggggaggaagtctcagaacactaccttttagtct 932
Qy 976 CATGAACCCGGTGAATCTAGCCCTTTGTGGAGAGAGGTTCGGGAAGTACCTCGGCCACTT 1035

Db 933 cttccaaaagcac 945
Qy 1036 CTTCCACAGGCAC 1048
RESULT 13
ID T76920 standard; cDNA; 1225 BP.
AC T76920;
DT 08-JUN-1998 (first entry)
DE DNA encoding human CC chemokine receptor 5 (CCR5).
KW CC chemokine receptor 5; CCR5; G-protein coupled receptor;
KW human immunodeficiency virus; HIV; CD4; AIDS; therapy;
KW transgenic animal; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 27..1085
FT /*tag= a
FT WO9745543-A2.
PD 04-DEC-1997.
PF 28-MAY-1997; U09586.
PR 28-MAY-1996; US-018508.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PI Alkhatib G, Berger EA, Broder CC, Combadiere C,
PI Feng Y, Kennedy PE, Murphy PM;
PI WPI: 98-032650/03.
DR P-PSDB; W23835.
PT CC chemokine receptor 5 polypeptide - used to inhibit membrane
PT fusion between HIV and a target cell
PS Claim 15; Fig 1C; 70pp; English.
CC This DNA sequence codes for a novel human macrophage-selective CC
CC chemokine receptor (see W23835) designated CCR5. It was isolated
CC from a lambda gill cDNA library. Another isolated DNA molecule (see
CC T76919) codes for an Alai27Leu variant (see W23834) of CCR5. The
CC susceptibility of human macrophages to HIV infection depends on
CC cell surface expression of the human CD4 molecule and CCR5. CCR5
CC is a member of the 7-transmembrane superfamily of G-protein
CC coupled cell surface molecules. It plays an essential role in the
CC membrane fusion step of infection by some HIV isolates. The
CC establishment of stable, non-human cell lines and transgenic
CC mammals having cells that coexpress human CD4 and CCR5 provides
CC valuable tools for research of HIV infection. Antibodies that bind
CC to CCR5, CCR5 variants, and CCR5-binding agents capable of blocking
CC membrane fusion between HIV and target cells represent potential
CC anti-HIV therapeutics for macrophage tropic strains of HIV.
CC Antisense oligonucleotides can also be used to inhibit expression
CC of CCR5 in a cell.
SQ Sequence 1225 BP; 289 A; 302 C; 280 G; 354 T;

Query Match 18.4%; Score 220; DB 39; Length 1225;
Best Local Similarity 65.3%; Pred. No. 1.44e-138;
Matches 556; Conservative 0; Mismatches 288; Indels 8; Gaps 7;

Db 124 tgcctccgctctactcaactggtgttcattcttgggtttgtgggcaacatgctggtcatcc 183
Qy 201 TGGCCCCGCTGTACTCCCTGGTGTTCACCTGTGGGCTCTTGGGCAATGTGGTGGTGA 260
Db 184 tcatctgataaaactgcaaaaggctgaagagcatgactgacatctacctgctcaactcgg 243
Qy 261 TGATCCTCATAAATACAGGAGGCTCCGAATATATGACCAACATCTACCTGTCAACCTGG 320
Db 244 ccactctgacctgttttcttcttactgtcccccttctgggctcaactatg-ctgcccgc 302
Qy 321 CCAATTCGAGCT 380
Db 303 c--agtgagacttggaaatacaatgctcaactcttgacagggctctattttatagct 360
Qy 381 ATACTGTGGTGTGGCCATGGCATGTGAAGCTCTCTCAGGGTTTATCACAGGCT 440
Db 361 tctctctggaatcttcttctcatctccctccctgacaactgtaggtacctggtcgtcgcc 420
Qy 441 TGTACAGGAGATCTTTTTCATATCTCTGTGTCATGACATCGACAGGTACCTTGCCATTGTC 500
Db 421 atgctgtgttctttaaagccaggaagcgtcaacttgggtggtgacagtgtatca 480

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ENTRY A57237 #type complete
TITLE chemokine (C-C) receptor 3 - human
ALTERNATE_NAMES C-C CKR-3
ORGANISM #formal_name Homo sapiens #common_name man
DATE 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change
29-Aug-1997
ACCESSIONS A57237
REFERENCE A57237
#authors Combadiere, C.; Ahuja, S.K.; Murphy, P.M.
#journal J. Biol. Chem. (1995) 270:16491-16494
#title Cloning and functional expression of a human eosinophil CC
chemokine receptor.
#accession A57237
##status preliminary; nucleic acid sequence not shown
##molecule_type mRNA
##residues 1-355 #label COM
##cross-references GB:028694
GENETICS
#gene GDB:CMKBR3
##cross-references GDB:579624; OMIM:601268
#map_position 3p21-3p21
#remarks 6 protein-coupled receptor; glycoprotein; phosphoprotein;
transmembrane protein
#feature
36-60 #domain transmembrane #status predicted #label TM1\
71-91 #domain transmembrane #status predicted #label TM2\
108-129 #domain transmembrane #status predicted #label TM3\
147-171 #domain transmembrane #status predicted #label TM4\
205-223 #domain transmembrane #status predicted #label TM5\
240-261 #domain transmembrane #status predicted #label TM6\
268-305 #domain transmembrane #status predicted #label TM7\
24-272,106-183 #disulfide_bonds #status predicted\
345 #binding_site phosphate (Ser) (covalent) (by casein
kinase II) #status predicted
SUMMARY #length 355 #molecular_weight 41072 #checksum 897
Query Match 98.74; Score 2729; DB 2; Length 355;
Best Local Similarity 98.9%; Pred. No. 0.00e+00;
Matches 351; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Db 1 MTSLSDTVEFTGTSYYDDVGLCEKADTRALMAQFVPLYSIVFTVGLGNVVMILI 60
Qy 1 MTSLSDTVEFTGTSYYDDVGLCEKADTRALMAQFVPLYSIVFTVGLGNVVMILI 60
Db 61 KRRRLRIMNITILNLAIISDLFLVTLRFVIRYVGHNMVFGHGMCKNLISGFYHGLYSE 120
Qy 61 KRRRLRIMNITILNLAIISDLFLVTLRFVIRYVGHNMVFGHGMCKNLISGFYHGLYSE 120
Db 121 IFFIILITDRILAIYHAFVALRARTVFGVITSTVWGLAVLAALPEFIETETELFE 180
Qy 121 IFFIILITDRILAIYHAFVALRARTVFGVITSTVWGLAVLAALPEFIETETELFE 180
Db 181 TLCSALYPEDTVYSWRHFTLRKTFCLVPLLVMAICYTGIIKTLRCPSKKKYAIRL 240
Qy 181 TLCSALYPEDTVYSWRHFTLRKTFCLVPLLVMAICYTGIIKTLRCPSKKKYAIRL 240
Db 241 IIVYIAVFEIETPYVALILSSYOSILFGNDCERKHLDRVAVLYEVAIYSHCCNPYI 300
Qy 241 IIVYIAVFEIETPYVALILSSYOSILFGNDCERKHLDRVAVLYEVAIYSHCCNPYI 300
Db 301 YAFVGERFRKRYLRFHRLMLHGLRYIPFLPSEKLEKRTSSVSPSAEDELISIV 355
Qy 301 YAFVGERFRKRYLRFHRLMLHGLRYIPFLPSEKLEKRTSSVSPSAEDELISIV 355
RESULT 3
ENTRY 149341 #type complete
TITLE MTP-1 alpha receptor like-2 - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
28-Feb-1997
ACCESSIONS 149341
REFERENCE 149339

#authors Gao, J.L.; Murphy, P.M.
#journal J. Biol. Chem. (1995) 270:17494-17501
#title Cloning and differential tissue-specific expression of three
mouse beta chemokine receptor-like genes, including the
gene for a functional macrophage inflammatory protein-1
alpha receptor.
#cross-references MUID:95340546
#accession I49341
##status preliminary; translated from GB/EMBL/DBJ
##molecule_type DNA
##residues 1-359 #label RBS
##cross-references EMBL:U28406; NID:9881551; PID:9881552
SUMMARY #length 359 #molecular_weight 41857 #checksum 8333
Query Match 67.8%; Score 1874; DB 2; Length 359;
Best Local Similarity 68.5%; Pred. No. 2.08e-252;
Matches 239; Conservative 50; Mismatches 58; Indels 2; Gaps 2;
Db 12 VESFETPYEEMAPR-CEKVRKEIGSMILPPLYSIVFTIIGLGNMVMVILIKRKIQ 70
Qy 8 VETFGTISTY-IDVGLCEKADTRALMAQFVPLYSIVFTIIGLGNVVMILIKRRLR 66
Db 71 IMTNILNLAIISDLFLFTVPFWIHVYLMNMGFGHYCMKLSGFYALYSEIFITL 130
Qy 67 IMTNILNLAIISDLFLVTLRFVIRYVGHNMVFGHGMCKNLISGFYHGLYSEIFITL 126
Db 121 LTIDRYIAVAVRRLARVTFATITSITWGLAGLAALPEFIETETELFE 190
Qy 127 LTIDRYIAVAVRRLARVTFATITSITWGLAGLAALPEFIETETELFE 186
Db 191 YPEGEDSMKRFHRLRMIFGLALPLVAVVICYSGIITLRCNKKKRIIRLIFVMI 250
Qy 167 YPEDVIVYWRHFTLRKTFCLVPLLVMAICYTGIIKTLRCPSKKKYAIRLIFVMA 246
Db 251 VEFIFWTPYNNVLLFSAPHSFLETSCEQSKHLDLMAQVTEVIAVTHCCVNPVIAVGE 310
Qy 247 VEFIFWTPYNNVLLFSAPHSFLETSCEQSKHLDLMAQVTEVIAVTHCCVNPVIAVGE 306
Db 311 RFRKRLRFPHRNQVTFENIFQPLPGENGRITSSVSTGEDELISIV 359
Qy 307 RFRKRLRFPHRNQVTFENIFQPLPGENGRITSSVSTGEDELISIV 355
RESULT 4
ENTRY A45177 #type complete
TITLE chemokine (C-C) receptor 1 - human
ALTERNATE_NAMES C-C CKR-1; macrophage inflammatory protein-1-alpha receptor
ORGANISM #formal_name Homo sapiens #common_name man
DATE 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
10-Sep-1997
ACCESSIONS A45177; I55671
REFERENCE A45177
#authors Neote, K.; Digregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.
#journal Cell (1993) 72:415-425
#title Molecular cloning, functional expression, and signaling
characteristics of a C-C chemokine receptor.
#cross-references MUID:93161416
#accession A45177
##status preliminary; nucleic acid sequence not shown
##molecule_type mRNA
##residues 1-355 #label NEO
##cross-references GB:LI0918; NID:9292416; PID:9292417
##experimental_source HL60 cells
#note Sequence extracted from NCBI backbone (NCBIP:124876)
REFERENCE I55671
#authors Gao, J.
#journal J. Exp. Med. (1993) 177:1421-1427
#title Structure and functional expression of the human macrophage
inflammatory 1 alpha (MIP-1alpha)/RANTES receptor.
#cross-references MUID:93240122
#accession I55671
##status preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA


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Query Match      52.5%;   Score 1452;   DB 2;   Length 383;
Best Local Similarity 54.2%;   Pred. No. 4,19e-189;
Matches 173;   Conservative 70;   Mismatches 74;   Indels 2;   Gaps 2

Db      56 YEEBAP-CYSDPTRLAAQVAPALALVLEGLGILNLIIVITVIRYKIKNTLMLNLN 114
      17 YDDGGLCEKADRLALMAQFVFPPLSYLFTGGLGNYVVMILKRYRLIMINILNL 76
Db      115 AISDLFLTLTPFWMHYIGMYHDWTFGSLCKLRGVCYMSYQVFCITLLTVDRYLAV 174
      77 AISDLFLTLVLPFWIHVY-RGNHWFGHGMCCKLLSGEYHNTGLYSEIFILLTIDRYLAI 135
Db      175 VYATLAREFTVCGIVTCVCMPLAGLLSLPEPEFHODNCRNOCDDPYEEMSTNW 234
      136 VHAVFALRATVTEFGVITSTVWGLAVLAAPLPEFLFETELCSALYEDDVTYSW 195
Db      235 RRAHVAKIVMLSLLELIMAVCYVILIRRLRPRSKKKAIALILFVIAVAFVFWTPY 294
      196 RHFTLRMTFTCLVLPFLMALCYGIIITLLRCPSSKKRYAIRLILFVIAVAFIWTY 255
Db      295 NIVLLSTFPAHLNLQCALSSNLMALLITKRYATVHCCINPIYVAFVGEKFRRLHYR 354
      256 NVAILLSSYQSILFGNDCERTKHLDLVMLEVIAYSHCCNPNPIYAFVGERRRKYLRF 315
Db      355 FHRTVAILCKYIPFLSGD 373
      316 FHRLLMHGRYIPFLPSE 334

RESULT      9
ENTRY      JC2443      #type complete
TITLE      chemokine (C-C) receptor 2, splice form B - human
ALTERNATE_NAMES      C-C-CR-2; monocyte chemoattractant protein 1 receptor;
                        monocyte chemotactin 1 receptor
ORGANISM      #formal_name Homo sapiens #common_name man
DATE      21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change
                        10-Sep-1997
ACCESSIONS      JC2443; 138463
REFERENCE      Yamaegami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.
                        Biochem. Biophys. Res. Commun. (1994) 202:1156-1162
                        cDNA cloning and functional expression of a human monocyte
                        chemoattractant protein 1 receptor.
#accession      JC2443
#molecule_type mRNA
#residues      1-360 #label YAM
#cross-references DDBJ:D29984; NID:g531246; PID:d1006817; PID:g531247
REFERENCE
#authors      Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly,
                        A.J.; Coughlin, S.R.
#journal      Proc. Natl. Acad. Sci. U.S.A. (1994) 91:2752-2756
#title      Molecular cloning and functional expression of two monocyte
                        chemoattractant protein 1 receptors reveals alternate
                        splicing of the carboxyl-terminal tails.
#cross-references EMBL:U03905; NID:g472557; PID:g472558
GENETICS
#gene      GDB:CMKBR2
#cross-references GDB:337364; OMIM:601267
#map_position 3p21-3p21
KEYWORDS      alternative splicing; G protein-coupled receptor;
                        glycoprotein; transmembrane protein
FEATURE
43-70      #domain transmembrane #status predicted #label TM1\
81-100      #domain transmembrane #status predicted #label TM2\
115-136      #domain transmembrane #status predicted #label TM3\
154-178      #domain transmembrane #status predicted #label TM4\
207-226      #domain transmembrane #status predicted #label TM5\
244-268      #domain transmembrane #status predicted #label TM6\

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287-309 #domain transmembrane #status predicted #label TM\
14 #binding site carbohydrate (Asn) (covalent) #status
113-190 #disulfide_bonds #status predicted
SUMMARY #length 360 #molecular-weight 41063 #checksum 1732

Query Match 52.0%; Score 1438; DB 2; Length 360;
Best Local Similarity 53.4%; Pred. No. 5,17e-187;
Matches 183; Conservative 87; Mismatches 63; Indels 10; Gaps 8;

Db 21 TTFEDYDYGAPCHKFDVQKIGAOQLPRLYSLVIFGFGNMLVLLINCKKLKCLTDY 80
14 TSYXD-DVGLCEKADPRLMAQFVPLYSLVFTFGLLGVVVVMIKRRRLRINTNY 72
QY 81 LNLALSDLLFLTLPLMAHA-ANEMVFGNACKLFTGLYHIGYGGIFITLTDY 139
73 LNLALSDLLFLTLPLMAHA-ANEMVFGNACKLFTGLYHIGYGGIFITLTDY 132

Db 140 LAIVHAFALKARTVTFGVTSVITWLVAVFASVPGIIFTCQKEDSVYVCGPFP--R- 196
133 LAIVHAFALKARTVTFGVTSVITWLVAVFASVPGIIFTCQKEDSVYVCGPFP--R- 192
QY 197 -GMNHTIMRNILGLVPLLMVICYSGILKTLRCRNEKRRRAVFIITMYELF 255
193 YSMRHFTLMTIFCLVPLVMAICYGIKTLRCPK-KKRYKARLIFVIMAVFIF 251
QY 256 WTPYNYVILNTQER-FGLSNCESTSQLDAQVETLGMTHCCINPIIYAFVGEKFR 314
252 WTPYNYVILNTQER-FGLSNCESTSQLDAQVETLGMTHCCINPIIYAFVGEKFR 310
QY 315 YLSVFFRKHTTRKRCQCFYREYDGVSTNTPSGDEVS 357
311 YLHFFHRLMLHGRITPLPSEKLE-RTSVSPSTAPPELS 352

RESULT 10 149340 #type complete
ENTRY MIP-1 alpha receptor like-1 - mouse
TITLE MIP-1 alpha receptor like-1 - mouse
ORGANISM Mus musculus #common_name house mouse
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 28-Feb-1997

ACCESSIONS 149340
REFERENCE 149339
#authors Gao, J.L.; Murphy, P.M.
#journal J. Biol. Chem. (1995) 270:17494-17501
#title Cloning and differential tissue-specific expression of three mouse beta chemokine receptor-like genes, including the gene for a functional macrophage inflammatory protein-1 alpha receptor.
#cross-references MIM:95340546
#accession 149340
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-356 #label RES
#cross-references EMBL:U28405; NID:9881549; PID:9881550
SUMMARY #length 356 #molecular-weight 40934 #checksum 563

Query Match 51.8%; Score 1433; DB 2; Length 356;
Best Local Similarity 52.0%; Pred. No. 2,88e-186;
Matches 173; Conservative 78; Mismatches 80; Indels 2; Gaps 2;

Db 22 GFLCEINRAFGITVPTPLYSLVFIIGVGHVLLVLIQHRKLRNMSTIYFNTAISD 81
QY 21 GLICEKADPRLMAQFVPLYSLVFTFGLLGVVVVMIKRRRLRINTNY 80
Db 82 LVLSTLPLFVNDYIMKGMDFGNACKFVSGEYLLIGYSMEFITLTDYLAHVAVF 141
QY 81 LFLVTLPLFPIHIVRGHNWFGHCKLISGFYHTGYSIFITLTDYLAIVAAV 140
Db 142 ALBARVTFGIISSITWVLAALVSPCLVVF-KSOMEFVHTCRALILPKSLIRLRFQ 200
QY 141 ALBARVTFGIISSITWVLAALVSPCLVVF-KSOMEFVHTCRALILPKSLIRLRFQ 199

Db 201 ALTMNIGLILPLAMITCYTRINLVHRRPNKKRAVRLIFVITLPLAPYLLA 260
QY 200 TLMTEFCVPLPLVNAICYGIKTLRCPKRRKARLIFVIMAVFIFMTPTVNAI 259
Db 261 FVSAPEDVFTFSCLSQOVDLSIMTEALAYTHCCVNPVIVGVGRKRYLMOLFRRH 320
QY 260 LLSYSIIFGNDCEKTHLDMVLTEVIAVSHCCMNPVIAFVGERKRLRHFH 319
Db 321 TAITPLQMLPFLSEDRASARLPSTVEIEMS 353
QY 320 LMLHGRITPLPSEKLERTSSVSPSTAPPELS 352

RESULT 11 138450 #type complete
ENTRY chemokine (C-C) receptor 2, splice form A - human
TITLE C-C CKR-2; monocyte chemoattractant protein 1 receptor;
ALTERNATE_NAMES monocyte chemoattractant protein 1 receptor
ORGANISM Homo sapiens #common_name man
DATE 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 29-Aug-1997

ACCESSIONS 138450
REFERENCE A53477
#authors Charo, I.F.; Myers, S.U.; Herman, A.; Franci, C.; Connolly,
A.D.; Coughlin, S.R.
Proc. Natl. Acad. Sci. U.S.A. (1994) 91:2752-2756
#journal Molecular cloning and functional expression of two monocyte chemoattractant protein 1 receptors reveals alternate splicing of the carboxyl-terminal tails.
#cross-references MIM:94195821
#accession 138450
#status preliminary
#molecule_type mRNA
#residues 1-374 #label RES
#cross-references EMBL:U03882; NID:9472555; PID:9472556

GENETICS GDB:CKBR2
#gene
#cross-references GDB:337364; OMIM:601267
#map_position 3p21-3p21
KEYWORDS alternative splicing; G protein-coupled receptor;
glycoprotein; transmembrane protein

FEATURE 44-68 #domain transmembrane #status predicted #label TM1\
79-99 #domain transmembrane #status predicted #label TM2\
115-136 #domain transmembrane #status predicted #label TM3\
154-178 #domain transmembrane #status predicted #label TM4\
208-226 #domain transmembrane #status predicted #label TM5\
244-265 #domain transmembrane #status predicted #label TM6\
292-309 #domain transmembrane #status predicted #label TM7\
14 #binding site carbohydrate (Asn) (covalent) #status predicted

SUMMARY #length 374 #molecular-weight 41914 #checksum 5414

Query Match 48.9%; Score 1352; DB 2; Length 374;
Best Local Similarity 56.2%; Pred. No. 3,51e-174;
Matches 168; Conservative 72; Mismatches 50; Indels 9; Gaps 7;

Db 21 TTFEDYDYGAPCHKFDVQKIGAOQLPRLYSLVIFGFGNMLVLLINCKKLKCLTDY 80
QY 14 TSYXD-DVGLCEKADPRLMAQFVPLYSLVFTFGLLGVVVVMIKRRRLRINTNY 72
Db 81 LNLALSDLLFLTLPLMAHA-ANEMVFGNACKLFTGLYHIGYGGIFITLTDY 139
QY 73 LNLALSDLLFLTLPLMAHA-ANEMVFGNACKLFTGLYHIGYGGIFITLTDY 132
Db 140 LAIVHAFALKARTVTFGVTSVITWLVAVFASVPGIIFTCQKEDSVYVCGPFP--R- 196
QY 133 LAIVHAFALKARTVTFGVTSVITWLVAVFASVPGIIFTCQKEDSVYVCGPFP--R- 192
Db 197 -GMNHTIMRNILGLVPLLMVICYSGILKTLRCRNEKRRRAVFIITMYELF 255
QY 193 YSMRHFTLMTIFCLVPLVMAICYGIKTLRCPK-KKRYKARLIFVIMAVFIF 251

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Db 256 MTNNIVLLNTPOEF-EGLSNCESTSQDQAQVTEFLGHTCCINPIIYAFGEKFR 313
| | | | : | | | | : | | : | | | | | : | | : | | | | | | | | | | |
Oy 252 WPTNVALLTSYSYLIFG-NDCERTKRLDLVLVTEVIAYASHCCMNPVIAFGEKFR 309

RESULT 12
ENTRY A57160 #type complete
TITLE Chemokine (C-C) receptor 4 - human
ALTERNATE_NAMES C-C CKR-4
ORGANISM #formal_name Homo sapiens #common_name man
DATE 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 15-Aug-1997

ACCESSIONS A57160
REFERENCE A57160
AUTHORS Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.; Wells, T.N.C.
JOURNAL J. Biol. Chem. (1995) 270:19495-19500
#journal title Molecular cloning and functional expression of a novel CC chemokine receptor cDNA from a human basophilic cell line
#accession A57160
#status preliminary; not compared with conceptual translation
#molecule_type mRNA
#residues 1-360 ##label PCW
#crosso-references GB:X85740
#note source clone K5-5

GENETICS GDB:CMKBRA
#gene #crosso-references GDB:677463
#map_position 3p21-3p21
KEYWORDS G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein

FEATURE
40-65 #domain transmembrane #status predicted #label TM1\
76-97 #domain transmembrane #status predicted #label TM2\
112-133 #domain transmembrane #status predicted #label TM3\
151-175 #domain transmembrane #status predicted #label TM4\
208-226 #domain transmembrane #status predicted #label TM5\
243-264 #domain transmembrane #status predicted #label TM6\
291-308 #domain transmembrane #status predicted #label TM7\
29-226,110-187 #disulfide_bonds #status predicted
72,350 #binding_site phosphate (Ser) (covalent) (by casein kinase II) #status predicted\
145 #binding_site phosphate (Ser) (covalent) (by protein kinase C) #status predicted\
183,194 #binding_site carbohydrate (Asn) (covalent) #status predicted\
321 #binding_site phosphate (Thr) (covalent) (by protein kinase C) #status predicted

SUMMARY #length 360 #molecular_weight 41402 #checksum 4713
Very Match 45.4% Score 1256; DB 2: length 360; Best Local Similarity 45.9%; Pred. No. 6.85e-160; Matches 161; Conservative 83; Mismatches 102; Indels 5; Gaps 5;

Db 9 TTLE-SIYSNYLYESIPKPCREGIKAFGELPLPPLYSLVFEGILGNSVYLVEKY 67
| | | : | | : | | : | | | | | | | | | | | | | | | | |
Oy 3 TSLDVFETFGTSDYDDGLGCEKADRPALMAQCVPPLYSLVFEGILGNVVVMILIKY 62

Db 68 KRLSMDVYLLNALISDLFEVSLPFGGYAQQ-VYFGIGLCKMTSMATLVGFYSGIT 126
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 63 RRLRMNIYILLNALISDLFEVLTPFIHVRRHNMWFHGMCKLISGTYHGLVSEIF 122

Db 127 FVMMSIDRYLAIFYAVSLRAPRTLTGVTLSTFWASVAVASPGLFSCYERHHYT 186
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 123 FILITIDRYLAIFYAHVAPALRARVTGVTISYTWGLAVIALPELTFETELEEEL 162

Db 187 CRTXSLNST-TWKVSSLSEINIQLVYPLGIIMFCYSMIIRTLQHCNKENKNAAVM 245
| | | : | | : | | : | | | | | | | | | | | | | | | | |
Oy 183 CSAYPEDTVASWRHFHLRMTICVAPPLVMAICTGITKITLRPSKKRYAKAILIF 242

Db 246 AVVVLGCFMWPNIVLFFLEVLVEVLYQDCFTERYLDYAIAQTETLAFAVHCCLNPIY 305
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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QY	243	VIMAVFLEFMPYVAILLSYQSILFGNDCERKHLDMVLTEVIATSHCCMNPIVITA	302
Db	306	FLGEEKRYKYLQLEFKTCRGLEFVLCQYCGLLQIYSADTPSSSSYQSTMDHL	356
QY	303	FVGEERFKRYLRHFFHR-HLMLHLGRYIPFLPSEKLE-RTSSVSPSTAPEL	351
RESULT	13		
ENTRY	JC4587	#type complete	
TITLE	chemokine (C-C) receptor 4 - mouse		
ORGANISM	#formal_name Mus musculus #common_name house mouse		
DATE	08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 12-Dec-1997		
ACCESSIONS	JC4587		
REFERENCE	JC4587		
#authors	Hoogewerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.		
#journal	Biochem. Biophys. Res. Commun. (1996) 218:337-343		
#title	Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to murine and human CC CKR-4.		
#accession	JC4587		
#molecule_type	mRNA		
#residues	1-360 #label HOO		
#cross-references	EMBL:X90862; NID:g1167851; PID:el95632; PID:g1167852		
#experimental_source	thymus		
GENETICS			
#gene	CC CKR-4		
KEYWORDS	glycoprotein; phosphoprotein; receptor; thymus		
FEATURE			
2,183,194			
72,202,350	#binding_site carbohydrate (Asn) (covalent) #status predicted\		
145	#binding_site phosphate (Ser) (covalent) (by casein kinase II) #status predicted\		
321	#binding_site phosphate (Ser) (covalent) (by protein kinase C) #status predicted\		
	#binding_site phosphate (Thr) (covalent) (by protein kinase C) #status predicted		
SUMMARY	#length 360 #molecular_weight 41462 #checksum 7852		
Query Match	43.3%; score 1198; DB 2; length 360;		
Best Local Similarity	43.7%; Pred. No. 2,81e-151;		
Matches 150; Conservative	92; Mismatches 97; Indels 4; Gaps 4;		
Db	16 YNSYFFESMKPCTKEGKAFGEVFLPPLYSLEVLGLFGNSVYVLFKRYKRLKSMTD	75	
QY	11 FGTSYDYDVGLECEKADRTALMAQFVPRPLYSLEVTGLGNNVYVILIKRYRLRIMTN	70	
Db	76 VYLLNLASDLLFLVSLPFGMYAADO-WPFGGLCKIYVSMVLGVGSIFFIMLSMD	134	
QY	71 IYLLNLASDLLFLVTLPEFWIHVYRGNNWVFGHCKMLLSGFYHTGYSIEIFIILLTD	130	
Db	135 RYLAIVAHVFLSKARLTLYGYITSLIWSVAVFASLGLFSTCYTEHNTYCKTOYSVN	194	
QY	131 RYLAIVAHVFLRARRVYTFGYITSLIWSGLAVLAALPEFLFETLELFEETLSALYPED	190	
Db	195 ST-TWKVLSLEINVLGLLPLGLIMLEFWSMIKRTLOCHCKNEKKRNARVIFGVVVLFLG	253	
QY	191 IYVSRHPEHTLRMTIFCLVPLIYMAICYGGIIKTLTRCPSKKRYAIRLIFVIMAVFPI	250	
Db	254 FWTPIRVNVLFEITLVELEVLDCTLEKYLDDYAIDATDTLGFHCCCLNPVYIFFLGKFKR	313	
QY	251 FWTPIRVNVAIILSSQSILFGNDCERTHDLVLMVLEVIAYSHCCMNPVIYAFVGERFKR	310	
Db	314 YITOLFTRCGRLVLCRKHCDPLVYADMSMSSYSTOTVHDF	356	
QY	311 YLRHFFHR-HLMLHLGRYIPFLPSEKLEKRTSSV-SPSTAPEL	351	
RESULT	14		
ENTRY	JC5067	#type complete	
TITLE	G protein-coupled receptor CKR-11 - human		
ALTERNATE_NAMES	chemokine receptor-like protein TER1; GPR-CY6		
ORGANISM	#formal_name Homo sapiens #common_name man		

DATE 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 10-Sep-1997

ACCESSIONS 10-Sep-1997

REFERENCE JC5067; G02776; G02387

#authors Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.

#journal Biochem. Biophys. Res. Commun. (1996) 227:846-853

#title Molecular cloning and RNA expression of two new human chemokine receptor-like genes.

#accession JC5067

#molecule-type DNA

#residues 1-355 #label ZAB

#cross-references EMBL:Z79782; NID:91668735; PID:e264772; PID:91668736

REFERENCE H01714

#authors Napolitano, M.; Zingoni, A.; Bernardini, G.; Spinetti, G.; Rocchi, M.; Santoni, A.

#submission submitted to the EMBL Data Library, June 1996

#accession G02776

#status translated from GB/EMBL/DBD

#molecule-type DNA

#residues 1-355 #label NAP

#cross-references EMBL:U62556; NID:91468978; PID:91468979

REFERENCE H01154

#authors Bonner, T.I.

#submission submitted to the EMBL Data Library, January 1996

#accession G02387

#status preliminary; translated from GB/EMBL/DBD

#molecule-type DNA

#residues 1-355 #label BON

#cross-references EMBL:U45983; NID:91245057; PID:91245057

COMMENT This protein belongs to the family of beta chemokine receptors.

GENETICS

KEYWORDS TER1

FEATURES

36-63 G protein-coupled receptor; transmembrane protein

73-94

108-129

147-171

200-222

239-260

281-304

SUMMARY

Query Match 39.0%; Score 1079; DB 2; Length 355;

Best Local Similarity 39.1%; Pred. No. 1.17e-133;

Matches 133; Conservative 97; Mismatches 102; Indels 8; Gaps 6;

DB 1 MDYTLDSVTVDYPPDIFSSPCDAELIQTNGKLLANFYCLLPFSLGNSLVILV 60

QY 1 MTSLSLDFEFGTTSYDDV-GLICERADRALMAQFVPLYSLVFTFGLGNVVMIL 59

DB 61 VCKKLSITDVLNLAISDLFVFSFPROTYVLLDO-VWFGVMCKVVSFGFYIGFS 119

QY 60 IKRRRLRIMNITILNLAISDLFVTLVPRIKVRGNVNFVGHGCKLISGFIHTGLYS 119

DB 120 SMFEITLMSYDRLAVVAVYALKVRTIRMGSTLCLAVMLTAIATPLLVFYVASE-D 178

QY 120 EIFFIILLTDRLAIYHAFALRARVTVGSIVTWGLAVLAALPEFIYFTEELFE 179

DB 179 GVLCYSFYNOQL-KKIKITNFKMILGLIPTIFMFCYIKLHOLKRONHNKTKAI 237

QY 180 ETL-CSALYPEDVDYVSRHNFHTLMTFCVLPLVMAICYTGIIKTLRLCPSKKKYKAI 238

DB 238 RLVLIVIASLLFVNPVNVFLRLSHMHLDCGSIQOLTVATHTVEIISFTHCCVNP 297

QY 239 RLIVIAVAFPIFTPNVAILSSYSIIFGNCERTKHLDMVLTVEVIAISHCCMP 298

DB 298 VYAVGEKFKHLSEIFORSQOIFNYLGROMPRESCEK 337

QY 299 VYAVGEKFKHLSEIFORSQOIFNYLGROMPRESCEK 335

RESULT 15

ENTRY IS8186 #type complete

TITLE hypothetical G-protein coupled receptor - rat

ORGANISM #formal_name Rattus norvegicus #common_name Norway rat

DATE 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 30-May-1997

ACCESSIONS IS8186

REFERENCE IS8186

#authors Harrison, J.K.; Barber, C.M.; Lynch, K.R.

#journal Neurosci. Lett. (1994) 169:85-89

#title cDNA cloning of a G-protein-coupled receptor expressed in rat spinal cord and brain related to chemokine receptors.

#cross-references MIMD:94323113

#accession IS8186

#status preliminary; translated from GB/EMBL/DBD

#molecule-type mRNA

#residues 1-354 #label RES

#cross-references EMBL:U04808; NID:9439860; PID:9439861

KEYWORDS G protein-coupled receptor

SUMMARY #length 354 #molecular-weight 40327 #checksum 4478

Query Match 38.8%; Score 1074; DB 2; Length 354;

Best Local Similarity 45.2%; Pred. No. 6.42e-133;

Matches 140; Conservative 77; Mismatches 88; Indels 5; Gaps 4;

DB 15 YDSSAECYIGDIVAFGTIFLSTFYSLVTFPGLVNLLVLAALNRSKRSITDIYLLN 74

QY 17 YDVGGLCEKADRALMAQFVPLYSLVFTFGLGNVVMILIKYRRLRIMNITVLLN 76

DB 75 ALSDLFVATLPFWHTYLLSHE-GLNANCKLTARFFIGFEGIFITVISTDRLATV 133

QY 77 ALSDLFVATLPFWHTYLLSHE-GLNANCKLTARFFIGFEGIFITVISTDRLATV 136

DB 134 LAANSNNRTVQGVITISLGVMAAIVASPOPMFTKRKD--NECL-GD-YPEVLOEIMP 189

QY 137 HAVFALRARVTVGSIVTWGLAVLAALPEFIYFTEELFCALYPEDTYVSMR 196

DB 190 VLKSEVNIIGFVPLILNSFCYFRVRLPFSCKNKKARATILLLVYVFFLEPTPIN 249

QY 197 HFHTLRMTGIFCLVPLVMAICYTGIIKTLRLCPSKKKYKAIPLIVIMAVFIPTPN 256

DB 250 IVFELTKRYNFPSCGKMRDRLMALSTETVAFSGCCNPTVAFAGKFRRLRLX 309

QY 257 VALLLSSYSIIFGNCERTKHLDMVLTVEVIAISHCCMPVYAVGEKFKYLRHFF 316

DB 310 NKCLAVLCGR 319

QY 317 HRRLMHLGR 326

Search completed: Tue Dec 8 13:14:00 1998

Job time : 61 secs.

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QY 303 FVGEFRFRKYLRFHRLHMLHGRYIFLPSEKLERTSSVSPSTAPELSTVF 355

RESULT 2 PRELIMINARY; PRT: 359 AA.

ID 054814; PRELIMINARY; PRT: 359 AA.

AC 054814; PRELIMINARY; PRT: 359 AA.

DT 01-JUN-1998 (TREMBLREL. 06, CREATED)

DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)

DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)

DE CHEMOKINE RECEPTOR CCR3.

OS RATVUS NORVEGICUS (RAT).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; RODENTIA.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-WISTAR; TISSUE-SPLEEN;

RA JIANG Y., SALAFRANCA M.N., ADHIKARI S., XIA Y., PENG L., SONNTAG M.K.,

RA DELEBE C.M., PENNELL N.A., STREET W.J., HARRISON J.K.,

RA J. NEUROIMMUNOL. 0:0-0(1998).

DR EMBL: AF003954; G2897073; .

SO SEQUENCE 359 AA; 41643 MW; C1PC70CA CRC32;

Query Match 69.8%; Score 1926; DB 11; Length 359;

Best Local Similarity 68.8%; Pred. No. 2,35e-275;

Matches 243; Conservative 55; Mismatches 52; Indels 3; Gaps 3;

DB 8 LKTVETETTPYEWAPP-CEKYSIRRLGSLPPLYSVLFVGLGNMNVLLIKY 66

QY 5 LDTV-ETFGTISY-YDDVOLLCEKADTRALMAQFVPLTSLVFTGLGNVVMILIKY 62

DB 67 RLQJMTNTYLLNLASDLFLFTVFPWFHYVLMNMGHGMCKMISGLYLYLXSEIF 126

QY 63 RLRLMTNTYLLNLASDLFLFTVFPWFHYVLMNMGHGMCKMISGLYLYLXSEIF 122

DB 127 FILLTIDRYLAIVAVLALRATYTFATITSIITMGFAVLAALDEFIFESODNFGDLS 186

QY 123 FILLTIDRYLAIVAVLALRATYTFATITSIITMGFAVLAALDEFIFESODNFGDLS 182

DB 187 CSPRPEGEEDSWKRFHRLHMLHGRYIFLPSEKLERTSSVSPSTAPELSTVF 246

QY 183 CSALPEDETVYSWRHFLHMLHGRYIFLPSEKLERTSSVSPSTAPELSTVF 242

DB 247 VMVIEFTEFMPYVNLVLLSAFSTFLESCQSHLDLMAQVTEVITHHCCINPIIYA 306

QY 243 VIMAEFTEFMPYVNLVLLSAFSTFLESCQSHLDLMAQVTEVITHHCCINPIIYA 302

DB 307 FVGEFRFRKYLRFHRLHMLHGRYIFLPSEKLERTSSVSPSTAPELSTVF 359

QY 303 FVGEFRFRKYLRFHRLHMLHGRYIFLPSEKLERTSSVSPSTAPELSTVF 355

Query Match 54.2%; Score 1495; DB 6; Length 352;

Best Local Similarity 55.2%; Pred. No. 7.95e-207;

Matches 185; Conservative 84; Mismatches 57; Indels 9; Gaps 9;

DB 20 COKINGOIAARLLPPLYSVLFVGNILVLLINCKRLKSMPTDIYLLNLASDLF 79

QY 24 CEKADTRALMAQFVPLYSVLFVGLGNVVMILIKYRLRLMTNTYLLNLASDLF 83

DB 80 LLTPFMAHYAAAO-WDEGNTMQLTGLTGFIFGFSGIFILLTIDRYLAIVAVALK 138

QY 84 LVTLPFWIHYVGRHNMVGHGMCKLISGFYTGTXSEIFILLTIDRYLAIVAVALK 143

DB 139 ARTYFGVTVSVITWVAVFASLPGIIFTRSORGLHYT-CSPHFPSQ-YQFKNQTL 196

QY 144 ARTYFGVTVSVITWVAVFASLPGIIFTRSORGLHYT-CSPHFPSQ-YQFKNQTL 201

DB 197 KAVILGLVPLVNAVIGSGILTKTLRCRNEKRRHRAVRLFTITMYVFLFMAVYNVL 256

QY 202 RMTIFGLVPLVNAVIGSGILTKTLRCRNEKRRHRAVRLFTITMYVFLFMAVYNVL 260

DB 257 LNTFOEF-FGLNCCSSNRLDQAMQVTELTGTHCCINPIIYAFVGEKFRNYLLVFEQKH 315

QY 261 LSSYOSILFG-NDCERSKHLDMVLTVEVIAVSHCCMNPVYAVGFRFRKYLHFRH 319

DB 316 IAKRFCKCSIFQOAPRASSVYTRSTGEDEISV 350

QY 320 LLMHGRYIFLPSEKLERTSSV-SPSTAPELSTVF 353

Query Match 54.4%; Score 1502; DB 6; Length 352;

Best Local Similarity 55.2%; Pred. No. 6.19e-208;

Matches 185; Conservative 83; Mismatches 58; Indels 9; Gaps 9;

DB 20 COKINGOIAARLLPPLYSVLFVGNILVLLINCKRLKSMPTDIYLLNLASDLF 79

QY 24 CEKADTRALMAQFVPLYSVLFVGLGNVVMILIKYRLRLMTNTYLLNLASDLF 83

DB 80 LLTPFMAHYAAAO-WDEGNTMQLTGLTGFIFGFSGIFILLTIDRYLAIVAVALK 138

QY 84 LVTLPFWIHYVGRHNMVGHGMCKLISGFYTGTXSEIFILLTIDRYLAIVAVALK 143

DB 139 ARTYFGVTVSVITWVAVFASLPGIIFTRSORGLHYT-CSPHFPSQ-YQFKNQTL 196

QY 144 ARTYFGVTVSVITWVAVFASLPGIIFTRSORGLHYT-CSPHFPSQ-YQFKNQTL 201

DB 197 KAVILGLVPLVNAVIGSGILTKTLRCRNEKRRHRAVRLFTITMYVFLFMAVYNVL 256

QY 202 RMTIFGLVPLVNAVIGSGILTKTLRCRNEKRRHRAVRLFTITMYVFLFMAVYNVL 260

DB 257 LNTFOEF-FGLNCCSSNRLDQAMQVTELTGTHCCINPIIYAFVGEKFRNYLLVFEQKH 315

QY 261 LSSYOSILFG-NDCERSKHLDMVLTVEVIAVSHCCMNPVYAVGFRFRKYLHFRH 319

DB 316 IAKRFCKCSIFQOAPRASSVYTRSTGEDEISV 350

QY 320 LLMHGRYIFLPSEKLERTSSV-SPSTAPELSTVF 353

[illegible]

RESULT	8		
ID	015538	PRELIMINARY;	PRT; 352 AA
AC	015538;		
DT	01-JAN-1998 (TREMPLREL, 05, CREATED)		

Db	20	COIKINVKQIARLRLPRLYSLVFTIGFNGNMVLIIILNCKRLKSMTDIYLLNLAINSLFF	79
QY	24	CEKADTRALMAQFVPPPLSVFTVGLLGNVVMILIKRYRLRLMTNITLYLLNLAIISDLF	83
Db	80	LLTVFPMHYAAAO-WMDGNMTCOLLGLGYIGFSGIFFIILLTDIRYLAIVAAVPAK	138
QY	84	LVTLPEFMHYHRYGHNWVFGHCKMLLSGFIHTGTGYSIELSEFIILLTDIRYLAIVAAVPAK	143
Db	139	ARTVTEGVTIVTVMVAVAFASLPGIIFTRSRQKGLHYTCSHPPEYSQ-YQFMKNFOTLK	197
QY	144	ARTVTEGVTIVTVMWGLAVLALAEPIFYETDELEFEELISGALPLDEDTYVS-WHHEFTLR	202
Db	198	IYVIGLVPLLVNVCISGILIKTLRCNEKKRRHRAVRLFTIMIVYFLFWAPYIVLL	257
QY	203	MTICVLVPLLVMAICYGTIKTLRCPS-KKKYKAIRLFIIVMAVFFIEMTPYNAVL	261
Db	258	NTPQEF-FGLNCCSSNNLDQAOVTELGMTROCCINPIYAFGEKFRNTLVLFPOKH	316
QY	262	SSYSIIFG-NDCKRSKHLDMVLTVEVIAHSCMNPVIAVAFGERFRKRLRHFHRHL	320
Db	317	AKRFKCCSIFQOEAPEPASSVYTRSGEOTISV	350
QY	321	LMHLGRYIFPLPSEKLERTSSV-SPSTAREPLST	353
RESULT	10		
ID	018772	PRELIMINARY;	PRT; 352 AA.
AC	018772		
DT	01-JAN-1998 (TREMBLREL. 05, CREATED)		
DT	01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)		
DT	01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)		
DE	CCRS RECEPTOR (FRAGMENT).		
GN	CCRS.		
OS	PAN TROGLODYTES (CHIMPANZEE).		
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;		
CC	EUTHERIA; PRIMATES.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=CHCR5-142A;		
RA	ZHANG L., CAROTHERS C.D., HE T., HUANG Y., CAO Y., WANG G., HAHN B.,		
RA	HO D.D.,		
RL	AIDS RES. HUM. RETROVIRUSES 0:0-0(1997).		
DR	EMBL; AF011541; G2305200; -		
DR	PFAM; PF00001; 7tm_1.		
DR	NON TER	352	
FT	SEQUENCE	352 AA; 40598 MW; A9BPEDEP CRC32;	
SO			
Query Match	53.5%;	Score 1477;	DB 6; Length 352;
Best Local Similarity	54.0%;	Pred. No. 5.63e-204;	
Matches 181; Conservative	87;	Mismatches 58;	Indels 9; Gaps 9;
Db	20	COIKINVKQIARLRLPRLYSLVFTIGFNDNMVLIIILNCKRLKSMTDIYLLNLAIISDLF	79
QY	24	CEKADTRALMAQFVPPPLSVFTVGLLGNVVMILIKRYRLRLMTNITLYLLNLAIISDLF	83
Db	80	LLTVFPMHYAAAO-WMDGNMTCOLLGLGYIGFSGIFFIILLTDIRYLAIVAAVPAK	138
QY	84	LVTLPEFMHYHRYGHNWVFGHCKMLLSGFIHTGTGYSIELSEFIILLTDIRYLAIVAAVPAK	143
Db	139	ARTVTEGVTIVTVMVAVAFASLPGIIFTRSRQKGLHYT-CSHFPYSQ-YQFMKNFOTL	196
QY	144	ARTVTEGVTIVTVMWGLAVLALAEPIFYETDELEFEELISGALPLDEDTYVS-WRHPHTL	201
Db	197	KIVVIGLVPLLVNVCISGILIKTLRCNEKKRRHRAVRLFTIMIVYFLFWAPYIVLL	256
QY	202	RMTIFCVLPLLVMAICYGTIKTLRCPS-KKKYKAIRLFIIVMAVFFIEMTPYNAVL	260
Db	257	LNTPOEF-FGLNCCSSNNLDQAOVTELGMTROCCINPIYAFGEKFRNTLVLFPOKH	315
QY	261	LSTYSIIFG-NDCKRSKHLDMVLTVEVIAHSCMNPVIAVAFGERFRKRLRHFHRH	319
Db	316	IAKRFKCCSIFQOEAPEPASSVYTRSGEOTISV	350

QY 320 LHMHLGRYIFLPSEKLERISV-SPSTAPELST 353

RESULT 11 PRELIMINARY: PRT: 352 AA.

AC 062743: 01-AUG-1998 (TREMBLREL. 07, CREATED)
DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
DE 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
BT CHEMOKINE RECEPTOR CCR5.
OS CEROCCEUS TOSOUATUS ATYS (RED-CROWNED MANGABEY).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA.
RN EUTHERIA; PRIMATES.
RP [1]
SEQUENCE FROM N.A.
CHEN Z., GETTIE A., HO D.D., MARX P.A.;
VIRIOLOGY 0:0-0(1998).

EMBL: AF051902; G3135296; -
SQ SEQUENCE 352 AA: 40407 MW: 1716C5C CRC32:

Query Match 53.3%; Score 1471; DB 6; Length 352;
Best Local Similarity 54.6%; Pred. No. 5,02e-203;
Matches 183; Conservative 84; Mismatches 59; Indels 9; Gaps 9;

DB 20 COKINAKQIARLLPPLYSLVIFGVGNILVLLINCKRKSMTDIYLNLAISDLF 79

QY 24 CERADTRALMAQFVPLYSLVFTGVLGNVVMILIKYRIMINILNLAIISDLF 83

DB 80 LUTVPMANHYAANO-WDFGTRCOLLTGLYFIFGSGIFILLTIDRYATAYHAGFALK 138

QY 84 LUTLPMHIVRHGNWFGHGMCKLISGFHTGLYSEIFILLTIDRYATAYHAGFALK 143

DB 139 ARTVEGVVSVITWVAVFASPLIFTRSGREGLHYT-CSPHFYSQ-YOFKMFQTL 196

QY 144 ARVTGVSITWGLAVLAALPEFIYETE-ELFEETICSLAYEDYYS-WRHFHTL 201

DB 197 KIVILGLVPLVAVICYSIGILKTLRCNKRKRRAVRLTIIMTYLFEMAYNIVLL 256

QY 202 RMTIFCLVPLVMAICYGTGIKTLRCPG-KKKYKARILFIYIMAVFIFMTPYNAVIL 260

DB 257 LNTFOEF-TGLNCCSSNRDQAMOTETIGMHCCINPIIYAFGEKFNILVFEQKH 315

QY 261 LSSYQISILFG-NCCERSKHLDMVLVTEVYAYSHCCMPYIYAFGEKFRKYLHFEFHRH 319

QY 316 IAKRFCKCSIFQOEASERASVYIRSTGEOEISV 350

QY 320 LHMHLGRYIFLPSEKLERISV-SPSTAPELST 353

RESULT 12 PRELIMINARY: PRT: 383 AA.

ID 089609: 01-NOV-1996 (TREMBLREL. 01, CREATED)

AC 089609: 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)

DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)

DE G PROTEIN-COUPLED RECEPTOR.

OS EQUINE HERPESVIRUS TYPE 2 (EHV-2).

OC VIRIDAE; DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE; ALPHAHERPESVIRINAE.

RN [1]

SEQUENCE FROM N.A.

RC STRAIN-86/67;

RA TELFORD E.A.R.;

RL SUBMITTED (FEB-1995) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: U20824; G695251; -

DR EMBL: U20824; G695173; -

DR PFAM: PF00001; 7tm_1.

SQ SEQUENCE 383 AA: 43667 MW: 6055BFD4 CRC32:

Query Match 52.2%; Score 1440; DB 14; Length 383;
Best Local Similarity 54.2%; Pred. No. 4,04e-198;
Matches 173; Conservative 69; Mismatches 75; Indels 2; Gaps 2;

DB 56 YEESAP-CYKSTITLAAQVAVLALVFLGGLGNILVIVIKIKITNLNL 114

QY 17 YDDVGLCKADTRALMAQFVPLYSLVFTGVLGNVVMILIKYRIMINILNL 76

DB 115 AISDLEFLTLPEFMHYGMVDMTFEGISICKLGVCMYSYOVFCITLTVRYAV 174

QY 77 AISDLEFLTLPEFMHYV-RGNWVFGHGMCKLSGFHTGLYSEIFILLTIDRYAL 135

DB 175 VYAVTALREFRYTCIVCVCTWFLAGLSLPEFFGHODNGVOCDPYXENSTWV 234

QY 136 VHAVFALRARTVTFGYITSIVTWGLAVLAALPEFIEFEELFEETICSLALPEDTVSW 195

DB 235 RRAHYAKVIMSLIPLIMAVCYIIRLLRPSKKYKARILFIYIMAVFYFWPY 294

QY 196 RHFHTLRMTIFCLVPLVMAICYGTGIKTLRCPGKKYKARILFIYIMAVFYFWPY 255

DB 295 NVILISTFHTLNLQCALSSNLMLALITKTVAYTHCCINPVIYAFGEKFRHLYH 354

QY 256 NVAILSSYQISILFGNDCRSKHLDMVLVTEVYAYSHCCMPYIYAFGEKFRKYLH 315

DB 355 FHTYVAIYLCYIFPLSGD 373

QY 316 FHRHLMHLGRYIFLPSE 334

RESULT 13 PRELIMINARY: PRT: 360 AA.

ID 018793: 01-JAN-1998 (TREMBLREL. 05, CREATED)

AC 018793: 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)

DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)

DE CHEMOKINE RECEPTOR.

GN CCR2B.

OS MACACA MULATTA (RHESUS MACAQUE).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA.

RN EUTHERIA; PRIMATES.

RP [1]

SEQUENCE FROM N.A.

RA HAVER D.A., MARGULIES B.J., CLEMENTS J.E.;

RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: AF013958; G2317748; -

DR PFAM: PF00001; 7tm_1.

SQ SEQUENCE 360 AA: 41111 MW: 13A47E2E CRC32:

Query Match 51.6%; Score 1425; DB 6; Length 360;
Best Local Similarity 53.4%; Pred. No. 9,52e-196;
Matches 183; Conservative 86; Mismatches 64; Indels 10; Gaps 8;

DB 21 TTFEDYDAPCHKREDVQIGAQLLPPLYSLVIFGVGNMLVLLINCKRKSITLDY 80

QY 14 TSYVD-DVGLCEKADTRALMAQFVPLYSLVFTGVLGNVVMILIKYRIMINIL 72

DB 81 LNLALISDLFLTLPLMAHSA-ANEMVFGNMGKLFGLYHIGYIGFILLTIDRY 139

QY 73 LNLALISDLFLTLPLFPMHYGMVDMTFEGISICKLGVCMYSYOVFCITLTVRY 132

DB 140 LAIVHAFALRARTVTFGYITSIVTWGLAVLAALPEFIEFEELFEETICSLALPEDTV 192

QY 133 LAIVHAFALRARTVTFGYITSIVTWGLAVLAALPEFIEFEELFEETICSLALPEDTV 192

DB 197 -GNNFHTIRNITGLVPLVAVICYSIGILKTLRCNKRKRRAVRLTIIMTYLF 255

QY 193 YSWRHHTLRMTIFCLVPLVMAICYGTGIKTLRCPG-KKKYKARILFIYIMAVFY 251

DB 256 WTPYNAVILNLTFOEF-FGLSNCESTRQDQATVETIGMHCCINPIIYAFGEKFR 314

QY 252 WTPYNAVILNLTFOEF-FGLSNCESTRQDQATVETIGMHCCINPIIYAFGEKFR 310

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RA DRAGAN , GIACLOVE J., PAE A., POWELL E., SOLINSKY K.A., DESTIVA U.,
RA DIAZ-PEREZ S., ZHOU X., YU Y., WATANABE M., DOGGETT N., GARCIA D.,
RA SACRIPANT J.L.,
RL SUBMITTED (MAY-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP ANSARI-LARI M.A., LIU X.-M., GORRELL J.H., GIBBS R.A.;
RA SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RA FAN P., KYAW H., SU K., ZENG Z., AUGUSTUS M., CARTER K.C., LI Y.,
RL BIOCHEM. BIOPHYS. RES. COMMUN. 243:264-268(1998).
DR EMBL: U95626; G2104521; -.
DR EMBL: AF014958; G2305264; -.
DR EMBL: U97123; G2897071; -.
SQ PFAM; PF00001; 7tm_1.
SQ SEQUENCE 344 AA; 39529 MW; C87A6CB5 CRC32;

Query Match 34.0%; Score 938; DB 4; Length 344;
Best Local Similarity 45.0%; Pred. No. 2,57e-119;
Matches 135; Conservative 72; Mismatches 76; Indels 17; Gaps 122

Db 28 CDKYDAQALSAQLVPSICSAVFVIGVLDNLILVLLIKYKGLKRVENIYLNLAVSNLCF 87
QY 24 CEKADTRALMAQFVPPLXSLVFTVGLGNVYVMIILIKRRLRIMTNTIYLLNLAIISDLF 83

Db 88 LLLLPFWAH-A-G----GDMCKILGLYFVGLYSEFFNCLLTVORYLVFLHGNFFS 140
QY 84 LVTLPEWTHYVRGNWYFGHGMCKLISGEVHTGLYSEIFFILITIDRYLAIVH-AVF-A 141

Db 141 AR-RRVCGITSLVAVTAIALLPREVYVYKPMEDQKKCAFSRPLPADETF-WKH 198
QY 142 LRAFTVFEVGTSLVITGLAVLALPEFIY--ETEEI-PEETICSAIY-PEDEVYSMRH 197

Db 199 FLTKMNISVAVLPFLFETFLYVOMRKTLL-RFRQR-YSLFKLVFAIMVYFLMMWARYNI 256
QY 198 FHTLRMTIFCLVLPILVMAICYTGIIKTLRCPSKKRYKAIRLFVIMAVFLEWTPYNV 257

Db 257 AFLSTFEKHEHSLSDCKSSYNLDKSVHITKLIATTHCCINPLVAFLDGTFESKYLRCFH 316
QY 258 AILSSYSLIFGNDCKRSKHLDMVLVTEVIIVASHCCMNPVIAFVGERFRKYLRRHFH 317

Search completed: Tue Dec 8 13:17:52 1998
Job time : 88 secs.

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ch_p protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Dec 8 13:15:36 1998; MasPar time 11.15 Seconds
Tabular output not generated. 854.574 Million cell updates/sec

Title: >US-08-963-656-4
Description: (1-355) from US08963656.pep
Perfect Score: 2760
Sequence: 1 MTSLDIVETFGTSTYYDDV.....LERTSSVSPSTAEPLSIVE 355

Scoring table: PAM 150
Gap 11

Searched: 74019 seqs, 26840295 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swissprot

Statistics: Mean 50.467; Variance 121.099; scale 0.417

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	2760	100.0	355	1	CKR3_HUMAN C-C CHEMOKINE RECEPTOR	0.00e+00
2	2551	92.4	355	1	CKR3_CERAE C-C CHEMOKINE RECEPTOR	0.00e+00
3	2533	91.8	355	1	CKR3_MACMU C-C CHEMOKINE RECEPTOR	0.00e+00
4	1960	71.0	359	1	CKR3_MOUSE PROBABLE C-C CHEMOKINE	0.00e+00
5	1834	66.4	355	1	CKR1_HUMAN C-C CHEMOKINE RECEPTOR	1.89e-288
6	1723	62.4	355	1	CKR1_MACMU C-C CHEMOKINE RECEPTOR	6.66e-269
7	1718	62.2	355	1	CKR1_MOUSE C-C CHEMOKINE RECEPTOR	5.05e-268
8	1507	54.6	352	1	CKR5_MACMU C-C CHEMOKINE RECEPTOR	1.43e-221
9	1499	54.3	352	1	CKR5_CERAE C-C CHEMOKINE RECEPTOR	5.67e-231
10	1498	54.3	352	1	CKR5_PAPHA C-C CHEMOKINE RECEPTOR	2.14e-228
11	1492	54.1	354	1	CKR5_RAT C-C CHEMOKINE RECEPTOR	2.41e-228
12	1489	53.9	352	1	CKR5_GORGO C-C CHEMOKINE RECEPTOR	8.08e-228
13	1486	53.8	352	1	CKR5_MOUSE C-C CHEMOKINE RECEPTOR	1.21e-227
14	1485	53.8	352	1	CKR5_PANTR C-C CHEMOKINE RECEPTOR	2.71e-227
15	1484	53.8	352	1	CKR5_HUMAN C-C CHEMOKINE RECEPTOR	6.07e-227
16	1459	52.9	373	1	CKR2_MOUSE C-C CHEMOKINE RECEPTOR	1.45e-222
17	1439	52.1	374	1	CKR2_MOUSE C-C CHEMOKINE RECEPTOR	4.57e-219
18	1435	48.4	374	1	CKR2_HUMAN C-C CHEMOKINE RECEPTOR	6.78e-201
19	1243	45.0	350	1	CKR4_HUMAN C-C CHEMOKINE RECEPTOR	7.28e-185
20	1199	43.4	360	1	CKR4_MOUSE C-C CHEMOKINE RECEPTOR	3.26e-177
21	1067	38.7	355	1	CKR8_HUMAN C-C CHEMOKINE RECEPTOR	2.46e-154
22	1059	38.4	354	1	GPRD_RAT PROBABLE G PROTEIN-COU	5.94e-153
23	1016	36.8	353	1	CKR8_MOUSE C-C CHEMOKINE RECEPTOR	1.37e-145

RESULT	1	ALIGNMENTS
ID	CKR3_HUMAN	STANDARD: PRT: 355 AA.
AC	P51677: Q15748:	
DT	01-OCT-1996 (REL. 34, CREATED)	
DT	01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)	
DT	15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)	
DE	C-C CHEMOKINE RECEPTOR TYPE 3 (C-C CKR-3) (CCR-3)	
DE	(EOSINOPHIL EOTAXIN RECEPTOR).	
GN	CKR3	
OS	HOMO SAPIENS (HUMAN)	
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;	
OC	EUTHERIA; PRIMATES.	
RP	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE-MONOCYTES:	
RX	MEDLINE: 95348056	
RA	COMBADIERE C., AHUJA S.K., MURPHY P.M.;	
RL	J. BIOL. CHEM. 270:16491-16494(1995).	
RL	[2]	
RP	ERRATUM.	
RA	COMBADIERE C., AHUJA S.K., MURPHY P.M.;	
RL	J. BIOL. CHEM. 270:30235-30235(1995).	
RL	[3]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE: 96235044.	
RA	DAUGHERTY B.L., SICILIANO S.J., DEMARTINO J.A., MALKOWITZ L.;	
RL	SIROGINA A., SPRINGER M.S.;	
RL	J. EXP. MED. 183:2349-2354(1996).	
RL	[4]	
RP	SEQUENCE FROM N.A.	
RA	QIN S., POST T.W., WANG J., WU L., GERARD N.P., NEWMAN W.;	
RL	GERARD C., MACKAY C.R.;	
RL	SUBMITTED (AUG-1996) TO EMBL/GENBANK/DBJ DATA BANKS.	
RL	[5]	
RP	SEQUENCE FROM N.A.	
RA	XIAO L., WEISS S., GARI S., RUDOLPH D., HODGE T., LAL R.;	
RL	SUBMITTED (NOV-1997) TO EMBL/GENBANK/DBJ DATA BANKS.	
CC	- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO EOTAXIN,	
CC	MCP-3, MCP-4 AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY	
CC	INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.	
CC	- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.	
CC	- TISSUE SPECIFICITY: IN EOSINOPHILS AS WELL AS TRACE AMOUNTS IN	
CC	NEUTROPHILS AND MONOCYTES.	
CC	- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.	
DR	EMBL: U28684; G1199580; -	
DR	EMBL: U51241; G1480481; -	
DR	EMBL: U49727; G1477561; -	

DR EMBL: AF026535; G2582566; -
 DR GCRDB; GCR_0988; -
 DR GCRDB; GCR_1931; -
 DR GCRDB; GCR_1934; -
 DR GCRDB; GCR_1993; -
 DR GCRDB; GCR_2529; -
 DR MIM: 601268; -
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; 1.
 DR G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE.
 FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 35 62 1 (POTENTIAL).
 FT DOMAIN 63 72 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 73 93 2 (POTENTIAL).
 FT DOMAIN 94 107 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 108 129 3 (POTENTIAL).
 FT DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 147 171 4 (POTENTIAL).
 FT DOMAIN 172 203 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 204 223 5 (POTENTIAL).
 FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 240 264 6 (POTENTIAL).
 FT DOMAIN 265 281 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 282 305 7 (POTENTIAL).
 FT DOMAIN 306 355 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 106 183 BY SIMILARITY.
 FT CONFLICT 276 276 S->T (IN REF. 4).
 SQ SEQUENCE 355 AA; 41043 MW; EHL45247 CRC32;

Query Match
 Best Local Similarity 100.0%; Score 2760; DB 1; Length 355;
 Matches 355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MTSLDVTEFETGTSYDDVGLCEKADTRALMAQFVPLYSIVTVGLGNVVMILI 60
 QY 1 MTSLDVTEFETGTSYDDVGLCEKADTRALMAQFVPLYSIVTVGLGNVVMILI 60
 Db 61 KRRRLRMNINILNLALSDDLFLVLPFWIHVGHNVFSGMKLLSGFHTGLYSE 120
 QY 61 KRRRLRMNINILNLALSDDLFLVLPFWIHVGHNVFSGMKLLSGFHTGLYSE 120
 Db 121 IFFIILLTDRLAIVHAFALRARTVETGVTISVTWGLAVLALPEFIYETEELPEE 180
 QY 121 IFFIILLTDRLAIVHAFALRARTVETGVTISVTWGLAVLALPEFIYETEELPEE 180
 Db 181 TCSAIIYEDIVYSWRHFTLMTIFCLVPLLVMAICYTGIIKTLKCPSSKKRYAIRL 240
 QY 181 TCSAIIYEDIVYSWRHFTLMTIFCLVPLLVMAICYTGIIKTLKCPSSKKRYAIRL 240
 Db 241 IFVIMAVFIEMTPYVAVALLSYOSILFGNDCERSKHLDVMTVEVIAVSHCCNPIYI 300
 QY 241 IFVIMAVFIEMTPYVAVALLSYOSILFGNDCERSKHLDVMTVEVIAVSHCCNPIYI 300
 Db 301 VAFVGERFRKYLRFHFRHVLMLHGRYIPFLPSEKLERTSSVSPSTAPELCLIVF 355
 QY 301 VAFVGERFRKYLRFHFRHVLMLHGRYIPFLPSEKLERTSSVSPSTAPELCLIVF 355

RESULT 2
 ID CKR3_CERAE STANDARD; PRT; 355 AA.
 AC P56492;
 DT 15-JUL-1998 (REL. 36, CREATED)
 DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
 DE 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE C-C CHEMOKINE RECEPTOR TYPE 3 (C-C CKR-3) (CCR-3).
 GN CMKBR3.
 OS CEROPITHECUS AETHIOPS (GREEN MONKEY) (GRIVEN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA SOL N., TREBOUET C., GOMAS E., FERCHAL F., ALIZON M.;
 RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO EOTAXIN,

CC MCP-3, MCP-4 AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
 CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL: Y13775; E1191907; -
 DR GCRDB: GCR_2422; -
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; 1.
 DR G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE.
 FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 35 62 1 (POTENTIAL).
 FT DOMAIN 63 72 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 73 93 2 (POTENTIAL).
 FT DOMAIN 94 107 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 108 129 3 (POTENTIAL).
 FT DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 147 171 4 (POTENTIAL).
 FT DOMAIN 172 203 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 204 223 5 (POTENTIAL).
 FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 240 264 6 (POTENTIAL).
 FT DOMAIN 265 281 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 282 305 7 (POTENTIAL).
 FT DOMAIN 306 355 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 106 183 BY SIMILARITY.
 SQ SEQUENCE 355 AA; 40830 MW; AED65DF8 CRC32;

Query Match
 Best Local Similarity 92.4%; Score 2551; DB 1; Length 355;
 Matches 327; Conservative 15; Mismatches 13; Indels 0; Gaps 0;

Db 1 MTSLSYVTEFETGTSYDDVGLCEKADVAGALIAQFVPLYSIVTVGLGNVVMILI 60
 QY 1 MTSLSYVTEFETGTSYDDVGLCEKADVAGALIAQFVPLYSIVTVGLGNVVMILI 60
 Db 61 KRRRLRMNINILNLALSDDLFLVLPFWIHVGHNVFSGMKLLSGFHTGLYSE 120
 QY 61 KRRRLRMNINILNLALSDDLFLVLPFWIHVGHNVFSGMKLLSGFHTGLYSE 120
 Db 121 IFFIILLTDRLAIVHAFALRARTVETGVTISVTWGLAVLALPEFIYETEELPEE 180
 QY 121 IFFIILLTDRLAIVHAFALRARTVETGVTISVTWGLAVLALPEFIYETEELPEE 180
 Db 181 TCSAIIYEDIVYSWRHFTLMTIFCLVPLLVMAICYTGIIKTLKCPSSKKRYAIRL 240
 QY 181 TCSAIIYEDIVYSWRHFTLMTIFCLVPLLVMAICYTGIIKTLKCPSSKKRYAIRL 240
 Db 241 IFVIMAVFIEMTPYVAVALLSYOSILFGNDCERSKHLDVMTVEVIAVSHCCNPIYI 300
 QY 241 IFVIMAVFIEMTPYVAVALLSYOSILFGNDCERSKHLDVMTVEVIAVSHCCNPIYI 300
 Db 301 VAFVGERFRKYLRFHFRHVLMLHGRYIPFLPSEKLERTSSVSPSTAPELCLIVF 355
 QY 301 VAFVGERFRKYLRFHFRHVLMLHGRYIPFLPSEKLERTSSVSPSTAPELCLIVF 355

RESULT 3
 ID CKR3_MACMU STANDARD; PRT; 355 AA.
 AC P56483;
 DT 15-JUL-1998 (REL. 36, CREATED)
 DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
 DE 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE C-C CHEMOKINE RECEPTOR TYPE 3 (C-C CKR-3) (CCR-3).
 GN CMKBR3.
 OS MACACA MULATTA (RHESUS MACAQUE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA HAUSER D.A., MARGOLIES B.J., CLEMENTS J.E.;
 RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA SOL N., TREBOUET C., GOMAS E., FERCHAL F., ALIZON M.;

RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO EOTAXIN.
CC MCP-3, MCP-4 AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AF017283; G2407219; -
DR EMBL: Y13776; E1192545; -
DR GCRDB: GCR_2424; -
DR GCRDB: GCR_2469; -
DR PROSITE: PS00237; G-PROTEIN RECEPTOR; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE.
FT DOMAIN 1 34 1 (POTENTIAL).
FT TRANSMEM 35 62 1 (POTENTIAL).
FT DOMAIN 63 72 2 (POTENTIAL).
FT TRANSMEM 73 93 2 (POTENTIAL).
FT DOMAIN 94 107 3 (POTENTIAL).
FT TRANSMEM 108 129 3 (POTENTIAL).
FT DOMAIN 130 146 4 (POTENTIAL).
FT TRANSMEM 147 171 4 (POTENTIAL).
FT DOMAIN 172 203 5 (POTENTIAL).
FT TRANSMEM 204 223 5 (POTENTIAL).
FT DOMAIN 224 239 6 (POTENTIAL).
FT TRANSMEM 240 264 6 (POTENTIAL).
FT DOMAIN 265 281 7 (POTENTIAL).
FT TRANSMEM 282 305 7 (POTENTIAL).
FT DOMAIN 306 335 7 (POTENTIAL).
FT DISULFID 106 183 CYTOPLASMIC (POTENTIAL).
FT CONFLICT 180 180 BY SIMILARITY.
FT CONFLICT 202 202 K -> E (IN REF. 2).
SO SEQUENCE 355 AA; 40805 MW; A839CACE CRC32;.

Query Match 91.8%; Score 2533; DB 1; Length 355;
Best Local Similarity 91.3%; Pred. No. 0.00e+00;
Matches 324; Conservative 16; Mismatches 15; Indels 0; Gaps 0;

Db 1 MTSLSDFVEFGPTSYDDMGILCEKADVGALLAOPPLYSLVFMVGLGNVVMVILI 60
OY 1 MTSLSDFVEFGPTSYDDMGILCEKADVGALLAOPPLYSLVFMVGLGNVVMVILI 60
Db 61 KYRLRLIMTNIYLNLALISDLLEFETLPFWIHVYRERNVSHQMKVLSGFEYTGLYSE 120
OY 61 KYRLRLIMTNIYLNLALISDLLEFETLPFWIHVYRERNVSHQMKVLSGFEYTGLYSE 120
Db 121 IFFIILITDRYLAIVHAFALRALRVTFGVITISVTWGLAVLAALPEFIYEDELFE 180
OY 121 IFFIILITDRYLAIVHAFALRALRVTFGVITISVTWGLAVLAALPEFIYEDELFE 180
Db 181 TLCSAIPQOTVSMRHFHTLKTILCLAPLVMALCYGIITLRLCPSSKKYKAIRL 240
OY 181 TLCSAIPQOTVSMRHFHTLKTILCLAPLVMALCYGIITLRLCPSSKKYKAIRL 240
Db 241 IFYIMAVFEFFMPYNAIILISTQSVLFGDCEKSHLDLFLVATEVIAVSHCCNAPVI 300
OY 241 IFYIMAVFEFFMPYNAIILISTQSVLFGDCEKSHLDLFLVATEVIAVSHCCNAPVI 300
Db 301 YAFVGEFRKRYLRHFRHVLMLGKTYIPPLSEKLEKTSVSPSTAEPESLIVF 355
OY 301 YAFVGEFRKRYLRHFRHVLMLGKTYIPPLSEKLEKTSVSPSTAEPESLIVF 355

RESULT 4
ID CKR3_MOUSE STANDARD; PRT; 359 AA.
AC P51678;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE PROBABLE C-C CHEMOKINE RECEPTOR TYPE 3 (C-C-CKR-3) (CC-CKR-3) (CCR-3)
DE (MACROPHAGE INFLAMMATORY PROTEIN-1 ALPHA RECEPTOR-LIKE 2) (MIP-1 ALPHA
DE R12).
DE CCKBR3 OR CCKBR12.
OS MRS MUSCULUS (MOUSE).
OC EUKARIOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-129/SV;
RX MEDLINE: 96072806.
RA POST T.M., BOZIC C.R., ROTHENBERG M.E., LUSTER A.D., GERARD N.,
RA GERARD C.;
RJ IMMUNOL. 155:5299-5305(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-129/SV;
RX MEDLINE: 95340546.
RA GAO J.-L., MURPHY P.M.;
RJ BIOL. CHEM. 270:17494-17501(1995).
CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO EOTAXIN,
CC MCP-3, MCP-4 AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: DETECTED IN SKELETAL MUSCLE AND IN TRACE
CC AMOUNTS IN LEUKOCYTES.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: U29677; G1109784; -
DR EMBL: U28406; G1203801; -
DR GCRDB: GCR_1673; -
DR GCRDB: GCR_1695; -
DR MGD: MGI:104616; CCKBR12.
DR PROSITE: PS00237; G-PROTEIN RECEPTOR; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE.
FT DOMAIN 1 38 1 (POTENTIAL).
FT TRANSMEM 39 64 1 (POTENTIAL).
FT DOMAIN 65 68 2 (POTENTIAL).
FT TRANSMEM 69 95 2 (POTENTIAL).
FT DOMAIN 96 111 3 (POTENTIAL).
FT TRANSMEM 112 133 3 (POTENTIAL).
FT DOMAIN 134 150 4 (POTENTIAL).
FT TRANSMEM 151 175 4 (POTENTIAL).
FT DOMAIN 176 201 5 (POTENTIAL).
FT TRANSMEM 202 227 5 (POTENTIAL).
FT DOMAIN 228 243 6 (POTENTIAL).
FT TRANSMEM 244 268 6 (POTENTIAL).
FT DOMAIN 269 285 7 (POTENTIAL).
FT TRANSMEM 286 309 7 (POTENTIAL).
FT DOMAIN 310 359 7 (POTENTIAL).
FT DISULFID 110 187 CYTOPLASMIC (POTENTIAL).
FT CONFLICT 270 270 BY SIMILARITY.
SO SEQUENCE 359 AA; 41825 MW; 3D2A9F0D CRC32;.

Query Match 71.0%; Score 1960; DB 1; Length 359;
Best Local Similarity 70.5%; Pred. No. 0.00e+00;
Matches 246; Conservative 51; Mismatches 50; Indels 2; Gaps 2;

Db 12 VESFEPTPEYEWAPP-CEVRIKELGSWLPPLYSLVFIIGLGMVVLILIKRKIQ 70
OY 8 VEFEGTTSY-YDVGGLCEKADTRALMAOFVPLYSLVFVGLGNVVMVILI KRRLR 66
Db 71 IMNITVNLALISDLLEFETLPFWIHVYRERNVSHQMKVLSGFEYTGLYSEIFIIIL 130
OY 67 IMNITVNLALISDLLEFETLPFWIHVYRERNVSHQMKVLSGFEYTGLYSEIFIIIL 126
Db 131 LITDRYLAIVHAFALRALRVTFATITSTWGLAGLALPEFIHESODSCEFSQSPR 190
OY 127 LITDRYLAIVHAFALRALRVTFATITSTWGLAGLALPEFIHESODSCEFSQSPR 186
Db 191 YPEGEESMRKRFHRLRNINGLALPLLVNVCYSGIITKTLRCPNKKHKAIRLIFVMI 250
OY 187 YPEDDYVSMRHFHTLKTILCLAPLVMALCYGIITLRLCPSSKKYKAIRLIFVIMA 246
Db 251 VEFIFWTPYLVLLFSAFHTFLETSCEDSKHDLAMQVTEVIAVTHCCVNPYAVGGE 310
OY 247 VEFIFWTPYLVLLFSAFHTFLETSCEDSKHDLAMQVTEVIAVTHCCVNPYAVGGE 306
Db 311 RFKKHLRFHRLRNANVYLGKTYIPPLSEKLEKTSVSPSTAEPESLIVF 359
OY 311 RFKKHLRFHRLRNANVYLGKTYIPPLSEKLEKTSVSPSTAEPESLIVF 359

Query Match 62.4% Score 1723; DB 1; Length 355;
 Best Local Similarity 60.1% Pred. No. 6.66e-269;
 Matches 215; Conservative 69; Mismatches 68; Indels 6; Gaps 6;

DB 1 METP-MTTEDYDMDITFEEDGADATP-CHKVERAAILAQLPPLSLVFIQVGNLVILV 58
 1 MTSLSDTVEFFG-TTSY-YDVGLLCEKADTRALMAQFVPLSLVFTVGLGNVYVMIL 58
 OY 1 MTSLSDTVEFFG-TTSY-YDVGLLCEKADTRALMAQFVPLSLVFTVGLGNVYVMIL 58
 DB 59 LVOYKRLKNTNIIYLLNLASIDLLFTLPFLIYKSTDMIFGDAMCKLLSGFYTGLY 118
 OY 59 LKRYRLRMTNIIYLLNLASIDLLFTLPFLIYKSTDMIFGDAMCKLLSGFYTGLY 118
 DB 119 SEIFFIILLTIDRYLAIVHAFVFLARVTFYGVITSIIIMALLASSPIMATSKTQWNI 178
 OY 119 SEIFFIILLTIDRYLAIVHAFVFLARVTFYGVITSIIIMALLASSPIMATSKTQWNI 178
 DB 179 VRHS-CNHFPEYSPFOQMLFOALKNLFGVLVPLVMIYCVYGIIRKILRRPNEKSKS 237
 OY 178 FEETLOSALYEDPTVYSWRHFTLRMTIFGLVPLVMACTGIITKLRCPSKKRYKA 237
 DB 238 VRLIEYIMIFELFWTPYNLTETLSVQEFELTHLCEQNDLAMEVEIVANMHCYV 297
 OY 238 IRLIEYIMAFEFIFMTYPYNAILLSSYOSILFGNDCERSKHLDMLVTEVIAVSHCCMN 297
 DB 298 PVIYAAGEFRKRYLQOLFHRRAVHLYKMLPFLSGDRLEKSVSTPSGHELSAGF 355
 OY 298 PVIYAAGEFRKRYLQOLFHRRAVHLYKMLPFLSGDRLEKSVSTPSGHELSAGF 355
 OY 298 PVIYAAGEFRKRYLQOLFHRRAVHLYKMLPFLSGDRLEKSVSTPSGHELSAGF 355

RESULT 7
 ID CKRL MOUSE STANDARD; PRT; 355 AA.
 AC P51675;
 DT 01-OCT-1996 (REL. 34, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE C-C CHEMOKINE RECEPTOR TYPE 1 (C-C CKR-1) (CCR-1)
 DE (MACROPHAGE INFLAMMATORY PROTEIN-1 ALPHA RECEPTOR) (MIP-1ALPHA-R)
 DE (RANTES-R).
 GN CMKBR1.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-129/SV; TISSUE-PERITONEAL MACROPHAGE;
 RA MEDLINE: 96072806.
 RA POST T.W., BOZIC C.R., ROTHENBERG M.E., LUSTER A.D., GERARD N.,
 RA GERARD C.;
 RA J. IMMUNOL. 155:5299-5305(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA STRAIN-129/SV;
 RA MEDLINE: 95340546.
 RA GAO J.-L., MURPHY P.M.;
 RA J. BIOL. CHEM. 270:17494-17501(1995).
 CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1 ALPHA,
 CC RANTES, AND LESS EFFICIENTLY, TO MIP-1 BETA OR MCP-1 AND
 CC SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR
 CC CALCIUM IONS LEVEL. RESPONSIBLE FOR AFFECTING STEM CELL
 CC PROLIFERATION.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: DETECTED IN THE HEART, SPLEEN, LUNG,
 CC PERITONEAL EXUDATE CELLS AND LEUKOCYTES.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL: U29678; GI109786; -
 DR EMBL: U28404; G881548; -
 DR GCRDB: GCR_1672; -
 DR GCRDB: GCR_1696; -
 DR MGD: MGI:104618; CMKBR1.
 DR PROSITE: PS00237; G-PROTEIN RECEPTOR; 1.
 KM G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE.
 FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 35 60 1 (POTENTIAL).
 RN

Query Match 62.2% Score 1718; DB 1; Length 355;
 Best Local Similarity 58.1% Pred. No. 5.05e-268;
 Matches 207; Conservative 83; Mismatches 64; Indels 2; Gaps 2;

DB 1 MEIS-DFTBAYPTTPEFDYDSTPCOKTAVRAFGAGLPLSLVFIQVGNLVILV 59
 1 MTSLSDTVEFFG-TTSY-DVGLCEKADTRALMAQFVPLSLVFTVGLGNVYVMIL 59
 OY 1 MTSLSDTVEFFG-TTSY-DVGLCEKADTRALMAQFVPLSLVFTVGLGNVYVMIL 59
 DB 60 MOHRLQSMSTIYLFENLAVSDLVFLFPFWIDYKLDKDMIFGDAMCKLLSGFYTGLY 119
 OY 60 IKYRLRMTNIIYLLNLASIDLLFTLPFLIYKSTDMIFGDAMCKLLSGFYTGLY 119
 DB 120 EIFFIILLTIDRYLAIVHAFVFLARVTFYGVITSIIIMALLASSPIMATSKTQWNI 178
 OY 120 EIFFIILLTIDRYLAIVHAFVFLARVTFYGVITSIIIMALLASSPIMATSKTQWNI 178
 DB 180 HRTSPHFPYKSLQWKRQALNLGLILPLVVICYAGIIRILRRPSEKRYKAVR 239
 OY 180 EITCSALYEDPTVYSWRHFTLRMTIFGLVPLVMACTGIITKLRCPSKKRYKAIR 239
 DB 240 LIFATILFLPMTYPNLSVFSAPDVLFTNOCESKHLDMAMOTEVIAVTHCCVNDI 299
 OY 240 LIFVIMAFEFIFMTYPYNAILLSSYOSILFGNDCERSKHLDMLVTEVIAVSHCCMN 299
 DB 300 IYFVGEFRKRYLQOLFHRRAVHLYKMLPFLSGDRLEKSVSTPSGHELSAGF 355
 OY 300 IYFVGEFRKRYLQOLFHRRAVHLYKMLPFLSGDRLEKSVSTPSGHELSAGF 355

RESULT 8
 ID CKR5_MACMU STANDARD; PRT; 352 AA.
 AC P79436; 002746;
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CKR-5) (CCR-5) (CCR5).
 GN CMKBR5.
 OS MACACA MUTATTA (RHESUS MACAQUE), MACACA FASCICULARIS (CRAB EATING
 OS MACAQUE) (CYNOMOLGUS MONKEY), AND MACACA NEMESTRINA (PIG-TAILED
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA SPECIES-M. MUTATTA;
 RA MEDLINE: 97184592.
 RA MARCON L., CHOE H., MARTIN K.A., FARZAN M., PONATH P.D., WU L.,
 RA NEWMAN W., GERARD N., GERARD C., SODROSKI J.;
 RA J. VIROL. 71:2522-2527(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA SPECIES-M. MUTATTA; STRAIN-INDIAN MACAQUE;
 RA MEDLINE: 97213934.
 RA CHEN Z., ZHOU P., HO D.D., LANDAU N.R., MARX P.A.;
 RA J. VIROL. 71:2703-2714(1997).
 RN [3]

RP SEQUENCE FROM N.A.
RC SPECIES=M.MULATTA.
RA HAUER D.A., MARGOLIES B.J., CLEMENTS J.E.;
RL SUBMITTED (APR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
[4]
RP SEQUENCE FROM N.A.
RC SPECIES=M.MULATTA, M.FASCICULARIS, AND M.NEMESTRINA;
RA EDINGER A.L., AMEDEE A., MILLER K., DORANZ B.J., ENDRES M.,
RA SHARON M., SAMSON M., LU Z.H., CLEMENTS J.E., MURPHEY-CORB M.,
RA PEIDER S.C., PARMENTIER M., BRODER C.C., DONS R.W.;
RL PROC. NATL. ACAD. SCI. U.S.A. 94:4005-4010(1997).
CC -I- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC DIFFERENTIATION.
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC
CC
CC EMBL: U77672; G1850350; -;
CC EMBL: U73739; G1771981; -;
CC EMBL: U96762; G208633; -;
CC EMBL: AF005660; G2245614; -;
CC EMBL: AF005661; G2245616; -;
CC EMBL: AF005662; G2245618; -;
CC
CC GCRDB: GCR_1286; -;
CC GCRDB: GCR_1369; -;
CC GCRDB: GCR_1370; -;
CC GCRDB: GCR_1371; -;
CC GCRDB: GCR_1639; -;
CC GCRDB: GCR_1641; -;
CC
CC PROSITE: PS00237; G-PROTEIN RECEPTOR, 1.
CC
CC KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.
CC
CC FT DOMAIN 1 30
CC FT TRANSMEM 31 58
CC FT DOMAIN 59 68
CC FT TRANSMEM 69 89
CC FT DOMAIN 90 102
CC FT TRANSMEM 103 124
CC FT DOMAIN 125 141
CC FT TRANSMEM 142 166
CC FT DOMAIN 167 198
CC FT TRANSMEM 199 218
CC FT DOMAIN 219 235
CC FT TRANSMEM 236 260
CC FT DOMAIN 261 277
CC FT TRANSMEM 278 301
CC FT DOMAIN 302 352
CC FT DISULFID 101 178
CC FT CARBOHYD 268 268
CC FT CONFLICT 241 241
CC FT CONFLICT 292 292
CC
CC SQ SEQUENCE 352 AA; 40507 MW; 9E6826EC CRC32;
Query Match 54.6%; Score 1507; DB 1; Length 352;
Best Local Similarity 55.5%; Pred. No. 5,67e-231;
Matches 186; Conservative 83; Mismatches 57; Indels 9; Gaps 9;

DB 257 INTFOEF-FGLNCCSSNRDLQAMQVTELTGTCGCCIPITIAFYAGEKFRNYLVLFQKH 315
OY 261 LSSYSILFG-NDCCRSKHLDMVLMEVIAVSHCCNMPVIAAFGEFRRLRHFFRH 319
DB 316 IAKRCKCSIFQCAPARASSVYTRSGEOEISV 350
OY 320 LLMHLGRYIPFLPSKELRTSSV-SPSTAPELST 353
RESULT 9
ID CKR5 CERAE STANDARD: PRT: 352 AA.
AC P56493;
DT 15-JUL-1998 (REL. 36, CREATED)
DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CKR-5) (CC-CKR-5) (CCR5).
GN CKR5
OS CERCOPITHECUS AETHIOPS (GREEN MONKEY) (GRIVET).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RX MEDLINE; 98001367.
RA KUHMANN S.E., PLATT E.J., KOZAK S.L., KABAT D.;
RL J. VIROL. 71:8642-8656(1997).
CC -I- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC DIFFERENTIATION.
CC
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC
CC CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
CC EMBL: U83324; G2347108; -;
CC EMBL: U83325; G2347110; -;
CC
CC GCRDB: GCR_2465; -;
CC GCRDB: GCR_2466; -;
CC
CC PROSITE: PS00237; G-PROTEIN RECEPTOR, 1.
CC
CC KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; POLYMORPHISM.
CC
CC FT DOMAIN 1 30
CC FT TRANSMEM 31 58
CC FT DOMAIN 59 68
CC FT TRANSMEM 69 89
CC FT DOMAIN 90 102
CC FT TRANSMEM 103 124
CC FT DOMAIN 125 141
CC FT TRANSMEM 142 166
CC FT DOMAIN 167 198
CC FT TRANSMEM 199 218
CC FT DOMAIN 219 235
CC FT TRANSMEM 236 260
CC FT DOMAIN 261 277
CC FT TRANSMEM 278 301
CC FT DOMAIN 302 352
CC FT DISULFID 101 178
CC FT VARIANT 14 14
CC FT VARIANT 352 352
CC
CC SQ SEQUENCE 352 AA; 40561 MW; 9CA7E235 CRC32;
Query Match 54.3%; Score 1499; DB 1; Length 352;
Best Local Similarity 55.2%; Pred. No. 1.43e-229;
Matches 186; Conservative 83; Mismatches 59; Indels 9; Gaps 9;

[illegible]

FT	DOMAIN	302	352	CYTOPLASTIC (POTENTIAL)
FT	DISULFID	101	178	BY SIMILARITY.
SO	SEQUENCE	352 AA;	40515 MM;	0AD97B12 CXC32:
	Query Match	53.9%;	Score 1489;	DB 1; Length 352;
	Best Local Similarity	54.6%;	Pred. No. 8,08e-228;	
	Matches 183;	Conservative	87;	Mismatches 56; Indels 9; Gaps 9;
D	20	CQKNNVQIARLLRPLKSLVFTIGFPGNMVYIIILNCRKRKSMPTIYLNLAIISLFF	79	
Q	24	CEKADTRALMAQFPPPLYSLVFTYGLGNVVMVILIKYRLRLMTINILNLAIISDLF	83	
D	80	LLVPEFAHYAAAO-WPEGNTMCOLLGLYFISGFIFILTTIDRYAIYAHVAALK	138	
Q	84	LVLLPEFMHYRGNNWFGHGMCKLSGFHTGYSLEIFILTTIDRYAIYAHVAALK	143	
D	139	ARVTFGVTVSVIMWVAFAFLDGLIIFTSQKEGLYHT-CSSHFPYSQ-YQFKNFQTL	196	
Q	144	ARVTFPGVITISIVMGLAVLAALPELFEYDE-BLEFETLCSALPEDIYVS-WRHHTL	201	
D	197	KIVLLGLVPLLVNVCISGLIKTLRLCRNEKKRRAVRLFTIMVYFLFWADYIVL	256	
Q	202	RMTIFCVLPPLVMAICYGTGIKTLRCPS-KKVKYKAIRLFVIMAVFIFWEPYNAVIL	260	
D	257	LNTROEF-FGLNCCSSNRDLDAQVAIVETLGMTCCINPIYAVGSKFRNYLLVFEOKH	315	
Q	261	LSSYOSILFQ-NDKERKHLDLVNLVEVLAYSCHCCNMPVIAFVAGFRFRYLLHFFHRH	319	
D	316	IAKRFCKCISFQOEAPERASSVYTRSTGEOEISV	350	
Q	320	LMHLGRYIPPLPSEKLERTSSV-SPSTAEPELSI	353	
	RESULT 13			
ID	PKR5_MOUSE	STANDARD;	PRY;	354 AA.
AC	P51682;	Q61867;	P97405;	Q35313; P97308; Q35891;
DT	01-OCT-1996	(REL. 34,	CREATED)	
DT	15-JUL-1998	(REL. 36,	LAST ANNOTATION UPDATE)	
DT	15-JUL-1998	(REL. 36,	LAST ANNOTATION UPDATE)	
DE	C-C-CHEMOKINE RECEPTOR TYPE 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (MIP-1 ALPHA RECEPTOR).			
GN	CMKR5.			
OS	MUS MUSCULUS (MOUSE).			
OC	EUKARYOTA; METAFOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; RODENTIA.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-129/SVJ; TISSUE-SPLEEN;			
RX	MEDLINE; 96205938.			
RA	BOHNG L., GOSLING J., MONTECLARO F.S., LUSIS A.J., TSOU C.-L.,			
RA	CHARO I.F.;			
RL	J. BIOL. CHEM. 271:14445-14451(1996).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-C57BL/6 X CBA; TISSUE-THYMUS;			
RX	MEDLINE; 96278910.			
RA	MEYER A., COLE A.J., PROUDFOOT A.E.I., WELLS T.N.C., POWER C.A.;			
RL	J. BIOL. CHEM. 271:14445-14451(1996).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-129/OLA;			
RA	KUTIEL W.A., BECK M.A., DAWSON T.C., MAEDA N.;			
RL	SUBMITTED (DEC-1996) TO EMBL/GENBANK/DBJ DATA BANKS.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-C57BL/6, AND NIH/SWISS; TISSUE-LIVER, KIDNEY, AND SPLEEN;			
RX	KUHMAN S.E., PLATT E.J., KOZAK S.L., KABAT D.;			
RL	J. VIROL. 71:8642-8656(1997).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-129;			
RX	MEDLINE; 97404635.			

RA DORANZ B.J., LU Z.H., RUCKER J., ZHANG T.Y., SHARRON M., CEN Y.H.,
 RA WANG Z.X., GUO H.H., DU J.G., ACCAVITTI M.A., DOMS R.W., PEIPER S.C.,
 RL J. VIROL. 71:6305-6314(1997).
 RN [6]
 RP SEQUENCE FROM N.A.
 RA GUO B., KUNO K., HARADA A., MATSUSHIMA K.,
 RL SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
 CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
 CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: DETECTED IN MONOCYTE/MACROPHAGE CELL LINES,
 CC BUT NOT IN NONHEMATOPOIETIC CELL LINES.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL: U47036; G1237136; -
 DR EMBL: X94151; E218395; -
 DR EMBL: U68565; G1698716; -
 DR EMBL: U83327; G2347114; -
 DR EMBL: AF022990; G2444487; -
 DR EMBL: AF019772; G2431976; -
 DR EMBL: D83648; G1777330; -
 DR GCRDB: GCR_1150; -
 DR GCRDB: GCR_1645; -
 DR GCRDB: GCR_1656; -
 DR GCRDB: GCR_1729; -
 DR GCRDB: GCR_2448; -
 DR GCRDB: GCR_2540; -
 DR GCRDB: GCR_2554; -
 DR MGD: MGI:107182; CMKR5.
 DR PROSITE: PS00237; G-PROTEIN RECEPTOR; 1.
 DR G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; POLYMORPHISM.
 FT DOMAIN 1 32
 FT TRANSMEM 33 60
 FT DOMAIN 61 70
 FT TRANSMEM 71 91
 FT DOMAIN 92 104
 FT TRANSMEM 105 126
 FT DOMAIN 127 143
 FT TRANSMEM 144 168
 FT DOMAIN 169 200
 FT TRANSMEM 201 220
 FT DOMAIN 221 237
 FT TRANSMEM 238 262
 FT DOMAIN 263 279
 FT TRANSMEM 280 303
 FT DOMAIN 304 354
 FT DISULFID 103 180
 FT CARBOHYD 270 270
 FT VARIANT 11 11
 FT VARIANT 62 62
 FT VARIANT 66 66
 FT VARIANT 97 97
 FT VARIANT 109 109
 FT VARIANT 156 156
 FT VARIANT 160 160
 FT VARIANT 185 185
 FT VARIANT 213 213
 FT VARIANT 318 318
 FT VARIANT 337 337
 FT CONFLICT 3 3
 FT CONFLICT 80 80
 FT CONFLICT 190 190
 FT CONFLICT 208 208
 FT CONFLICT 145 145
 SO SEQUENCE 354 AA; 40863 MW; 6ECD306A CRC32;
 Query Match 53.98; Score 1488; DB 1; Length 354;
 Best Local Similarity 54.48; Pred. No. 1,21e-227;
 Matches 181; Conservative 82; Mismatches 63; Indels 7; Gaps 7;
 Db 22 COKINVAQIAQLPLPVSVIFGFGVGNMVFLLISCKLKSVGTIYLLNLAIISDLF 81
 Oy 24 CERKDTBALMAQFVPLXSLVFTYGLGNVYVWILIKRYRLRINTIYLLNLAIISDLF 83

Db 82 LLLPLPMAHYA-ANEMIFGNCKVTVGYHIGEGIFPIILLITDRYLAIVHAFALK 140
 Oy 84 LVPLPFWIHVYRGHNMVFGHGMCKLLSGFTYGLYSEIFILLITDRYLAIVHAFALR 143
 Db 141 VFTVNGVITSVTVVAVASAPLEIIFTRSOKEGHYT-CSPHPHYQVHFKPSQTLK 199
 Oy 144 ARVTVGVITSYTWGLAVIALPELIFYETE-ELDEETLCSLLYEDVYSRHHHTLR 202
 Db 200 MVLISLPLLVMIICYSGLIHTLFRCKRNEKRRHRAVRLFAIMYVFLFMPYNIYLL 259
 Oy 203 MTFELVLPPLVAVICVTGKITLLNCPG-KKKYKAIKLFVIMAVFIIWTFYNAIILL 261
 Db 260 TTRQEF-FGLNCCSSNRDLQAMQATETLGMHCCNPVYAVGEKRSYSVFFRKHI 318
 Oy 262 SSYOSILFV-NDCKRSKHDLVMLVTEVIAVSHCCNMPYVAVGERFRKYLHFFHRL 320
 Db 319 VKRCKRSIFQODNDPDRVSVYTRSTGEHVS 351
 Oy 321 LMHLGRITPPLPSEKLERTSV-SPSTAPELS 352
 RESULT 14
 ID CKR5_PANTR STANDARD; PRT; 352 AA.
 AC PS6440; 002778;
 DT 15-JUL-1998 (REL. 36, CREATED)
 DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
 GN CMKR5.
 OS PAN TROGLODYTES (CHIMPANZEE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 97268687.
 RA EDINGER A.L., AMEDEE A., MILLER K., DORANZ B.J., ENDRES M.,
 RA SHARRON M., SAMPSON M., LU Z.H., CLEMENTS J.E., MURPHY-CORB M.,
 RA PEIPER S.C., PARMENTIER M., BRODER C.C., DOMS R.W.,
 RA PROC. NATL. ACAD. SCI. U.S.A. 94:4005-4010(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA ZIMMERMAN P.A., BOCKLER-WHITE A., ALKHATTIB G.,
 RL SUBMITTED (MAR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 98022612.
 RA ZHANG L., CARROTHERS C.D., HE T., HUANG Y., CAO Y., WANG G., HAHN B.,
 RA HO D.D.,
 RL AIDS RES. HUM. RETROVIRUSES 13:1357-1366(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 97426118.
 RA ZACHAROVA V., ZACHAR V., GOUSTIN A.S.,
 RL AIDS RES. HUM. RETROVIRUSES 13:1159-1161(1997).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 98090115.
 RA PRETET J.-L., ZERBIB A., GIRARD M., GUILLET J.-G., BUTOR C.,
 RL AIDS RES. HUM. RETROVIRUSES 13:1583-1587(1997).
 CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
 CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
 CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
 CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
 CC DIFFERENTIATION.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL: AF005663; G2245620; -
 DR EMBL: U94329; G2145188; -
 DR EMBL: AF011542; G2305202; -
 DR EMBL: U97666; G2327059; -
 DR EMBL: AF011540; G2305198; -
 DR EMBL: U89797; G2281445; -


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DR GCRDB: GCR.1284;
DR GCRDB: GCR.1357;
DR GCRDB: GCR.2432;
DR PROSITE: PS00237; G-PROTEIN RECEPTOR; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 59 68 1 (POTENTIAL).
FT DOMAIN 69 89 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 90 102 2 (POTENTIAL).
FT DOMAIN 103 124 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 125 141 3 (POTENTIAL).
FT TRANSMEM 142 166 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 167 198 4 (POTENTIAL).
FT TRANSMEM 199 218 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 219 235 5 (POTENTIAL).
FT TRANSMEM 236 260 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 261 277 6 (POTENTIAL).
FT TRANSMEM 278 301 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 302 352 7 (POTENTIAL).
FT DISULFID 101 178 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 268 268 BY SIMILARITY.
FT CONFLICT 123 123 T -> S (IN REF. 1).
SEQUENCE 352 AA; 40539 MW; D6554684 CRC32;
Query Match 53.8%; Score 1486; DB 1; Length 352;
Best Local Similarity 54.6%; Pred. No. 2, 71e-227;
Matches 183; Conservative 86; Mismatches 57; Indels 9; Gaps 9;
DB 20 CCKINVKQIAALLPLPLYSVLFPGVGMVLILLINCKRLKSMDDIILNATISDFE 79
OY 24 CKAQDRAIMAFVPLPLSLVFTVGLGNVVMMILIKRRLIMINITYLLNATISDLF 83
DB 80 LITVEFMHAYAAQ-WDEGNTMCOILTGLYFGFSGIFILLIDRYLAIVHAFALK 138
OY 84 LVTLPFMHYVGHMNVFEGHGMCKILSGFYHGYSEIFILLIDRYLAIVHAFALK 143
DB 139 AATVTFGVTVITVNVAVFASLPGLIFTRSOKEGLHT-CSSHFYSO-YQFMKNFQL 196
OY 144 AATVTFGVTVITVNVAVFASLPGLIFTRSOKEGLHT-CSSHFYSO-YQFMKNFQL 201
DB 197 KVIILGLVPLLVNVCYSGILKTLRCNKKRRAVLFITMIVYLFNAPYIVLL 256
OY 202 RHTICLVPLVMAICYGIITKILRCS-KKKYALHIVYNAVFIEFIPVIAL 260
DB 257 LNTFOEF-FGLNCGSSNLDQAMOVETLGMTHCCINPIIYAFVGEKRNVLVFFQKH 315
OY 261 LSSYOSILFG-NDCEKSKHLDMVLTETVYAVSHCCMNPVYIAFVGERRKYLRHFFHH 319
DB 316 IAKRCKCCSIFQOEPAPERASSVYITSGEOELISV 350
OY 320 LLMHGRYIPFLPSEKLETTSSV-SPSTAEPELSI 353

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RX MEDLINE: 96291862.
RA RAPORT C.J., GOSLING J., SCHWEICHAUT V.L., GRAY P.W., CHARO I.F.;
RA J. BIOL. CHEM. 271:17161-17166(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE: 96295970.
RA COMBADIERE C., AUDA S.K., TIEFANY H.L., MURPHY P.M.;
RA J. LEUKOC. BIOL. 60:147-152(1996).
RN [4]
RP SEQUENCE FROM N.A.
RA MCCOMBIE W.R., WILSON R., CHEN E., GIBBS R., ZUO L., JOHNSON D.,
RA NHAN M., PARNELL L., DEHIA N., ANSARI A., MARDIS E., SCHUTZ K.,
RA GNOI L., LA BASTIDE M., KAPLAN N., GRECO T., TOUCHMAN J.,
RA MUZY D., CHEN C.N., EVANS C., FITZGERAID M., SEE L.H., TANG M.,
RA PORCEL B.M., DRAGAN Y., GIACALONE J., PAE A., POWELL E.,
RA SOLINSKY K.A., DESILVA U., DIAZ-PEREZ S., ZHOU X., YU Y.,
RA WATANABE M., DOGGETT N., GARCIA D., SAGRIPANTI J.L.;
RA SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDJ DATA BANKS.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE: 98001387.
RA KUHMANN S.E., PLATT E.J., KOZAK S.L., KABAT D.;
RA J. VIROL. 71:8642-8656(1997).
RN [6]
RP SEQUENCE FROM N.A. AND POLYMORPHISMS.
RX MEDLINE: 98022612.
RA ZHANG L., CARUTHERS C.D., HE T., HUANG Y., CAO Y., WANG G., HAHN B.,
RA HO D.D.;
RA AIDS RES. HUM. RETROVIRUSES 13:1357-1366(1997).
RN [7]
RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
RX MEDLINE: 96260017.
RA DENG H., LIU R., ELMETIER W., CHOE S., UNUTMAZ D., BURKHART M.,
RA DI MARZO P.C., MARMON S., SUTTON R.E., HILL C.M., DAVIS C.B.,
RA PEPPER S.C., SCHALL T.J., LITMAN D.R., LANDAU N.R.;
RA NATURE 381:661-666(1996).
RN [8]
RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
RX MEDLINE: 96260018.
RA DRAGIC T., LITWIN V., ALLAWAY G.P., MARTIN S.R., HUANG Y.,
RA NAGASHIMA K.A., CAVANAN C., MADDON P.J., KOUP R.A., MOORE J.P.,
RA PAYTON W.A.;
RA NATURE 381:667-673(1996).
RN [9]
RP FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
RX MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
RX INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
RX IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
RX DIFFERENTIATION.
CC -I- FUNCTION: ACTS AS AS CO-RECEPTOR WITH CD4 FOR PRIMARY NON-
CC SYNCYTUM-INDUCING STRAINS (NSI) (MACROPHAGE-TROPIC) OF HIV-1
CC VIRUS. IT PROMOTES ENV-MEDIATED FUSION OF THE VIRUS.
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -I- TISSUE SPECIFICITY: FOUND IN PROMYELOCYTIC CELLS.
CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
RN [10]
RP SEQUENCE FROM N.A.
RX MEDLINE: 91992877.
RA EMBL: X91492; E1992877;
RA EMBL: U54994; G1457946;
RA EMBL: U57840; G1502409;
RA EMBL: U95626; G2104520;
RA EMBL: U83326; G2347112;
RA EMBL: AF011500; G2305118;
RA EMBL: AF011501; G2305120;
RA EMBL: AF011502; G2305122;
RA EMBL: AF011503; G2305124;
RA EMBL: AF011505; G2305128;
RA EMBL: AF011506; G2305130;
RA EMBL: AF011507; G2305132;
RA EMBL: AF011508; G2305134;
RA EMBL: AF011509; G2305136;
RA EMBL: AF011510; G2305138;
RA EMBL: AF011511; G2305140;
RA EMBL: AF011512; G2305142;
RA EMBL: AF011513; G2305144;
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MISALIGNMENT
(TM)

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ch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Dec 8 13:18:11 1998; Maspar time 14.72 Seconds
Tabular output not generated. 823.402 Million cell updates/sec

Title: >US-08-963-656-4
Description: (1-355) from US08963656.pep
Perfect Score: 2760
Sequence: 1 MTSLDVTEFTGTSYYDDV.....LERTSSVSPSTAEPLSIVF 355

Scoring table: PAM 150
Gap 11

Searched: 107076 segs, 34141958 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir56
1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 48.858; Variance 137.386; scale 0.356

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	2758	99.9	355	2	C-C chemokine receptor	0.00e+00
2	2741	99.3	355	2	chemokine (C-C) recep	0.00e+00
3	1880	68.1	359	2	MIP-1 alpha receptor	1.45e-253
4	1834	66.4	355	2	chemokine (C-C) recep	1.23e-246
5	1723	62.4	355	2	macrophage inflammatory	6.19e-230
6	1484	53.8	352	2	CC chemokine receptor	3.13e-194
7	1484	53.8	352	2	chemokine (C-C) recep	4.41e-194
8	1440	52.2	383	2	G protein-coupled rec	1.69e-187
9	1439	52.1	356	2	MIP-1 alpha receptor	2.38e-187
10	1421	51.5	360	2	chemokine (C-C) recep	1.17e-184
11	1335	48.4	374	2	chemokine (C-C) recep	8.06e-172
12	1243	45.0	360	2	chemokine (C-C) recep	4.06e-158
13	1199	43.4	360	2	chemokine (C-C) recep	1.41e-151
14	1067	38.7	355	2	G protein-coupled rec	5.11e-132
15	1059	38.4	354	2	hypothetical G-protei	7.78e-131
16	1011	36.6	355	2	orphan G-protein-coup	9.45e-124
17	850	30.8	369	2	G protein-coupled rec	4.09e-100
18	825	29.9	378	2	lymphocyte-specific G	1.83e-96
19	796	28.8	378	2	G protein-coupled pep	3.07e-92
20	779	28.1	378	2	G protein-coupled rec	2.49e-89
21	739	26.8	360	2	interleukin-8 recepto	5.81e-84
22	726	26.3	350	2	interleukin-8 recepto	4.43e-82
23	719	26.1	352	2	leukocyte-derived sev	4.56e-81

24	716	25.9	355	2	J01231	interleukin-8 recepto	1.24e-80
25	710	25.7	352	2	G00048	fusin (LESTRA) - ctab	9.11e-80
26	699	25.3	358	2	A53752	interleukin-8 recepto	3.53e-78
27	691	25.0	353	2	S28787	neuropeptide Y/peptid	5.03e-77
28	670	24.3	374	2	S42628	G-protein coupled rec	5.33e-74
29	668	24.2	359	2	A42656	angiotensin II recept	1.03e-73
30	658	23.8	350	2	JN0621	G-protein coupled rec	2.83e-72
31	657	23.8	359	2	S44425	angiotensin II recept	3.94e-72
32	655	23.7	359	2	JC2134	angiotensin II recept	7.64e-72
33	654	23.7	359	2	J01516	angiotensin II recept	1.06e-71
34	652	23.6	356	2	S42096	interleukin-8 recepto	2.06e-71
35	652	23.6	359	2	JC1104	angiotensin II recept	2.06e-71
36	650	23.6	359	2	JH0621	angiotensin receptor	3.99e-71
37	650	23.6	359	2	A48921	interleukin-8 recepto	3.99e-71
38	649	23.5	374	2	S32785	G protein-coupled rec	5.55e-71
39	647	23.4	359	2	A48857	ATI angiotensin II re	1.08e-70
40	645	23.4	359	2	S15403	angiotensin II recept	2.08e-70
41	639	23.2	327	2	S56162	MDCK15 protein - huma	1.51e-69
42	639	23.2	372	2	S26667	G protein-coupled rec	1.51e-69
43	637	23.1	359	2	I51372	angiotensin receptor	2.92e-69
44	632	22.9	359	2	JC1193	angiotensin II recept	1.52e-68
45	630	22.8	362	2	JN0694	angiotensin II recept	2.94e-68

ALIGNMENTS

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	ORGANISM		#formal_name Homo sapiens #common_name man	
	DATE		21-Dec-1990 #sequence_revision 06-Jun-1997 #text_change 06-Jun-1997	

ACCESSIONS	G02436
REFERENCE	H01272
#authors	Ponath, P.D.
#submission	submitted to the EMBL Data Library, February 1996
#accession	G02436
#status	preliminary; translated from GB/EMBL/DBJ
#molecule_type	DNA
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##cross-references	EMBL:U49727; NID:g1477560; PID:g1477561
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QY	61	KYRRRLIMNTIYLNLAIISDLFLVTLPLWIVYVGHMNVFEGHCKLLSGYHGLYSE	120
DB	121	IFFIILITDRILAIYHAFALRARTVGTSTIYTWGLAVLAALPEFIETETLPEE	180
QY	121	IFFIILITDRILAIYHAFALRARTVGTSTIYTWGLAVLAALPEFIETETLPEE	180
DB	181	TLCASALYPEDTVYSWRHFTLMTIFCLVPLLVNAICVTGIITKLRLCPSSKKYKAI	240
QY	181	TLCASALYPEDTVYSWRHFTLMTIFCLVPLLVNAICVTGIITKLRLCPSSKKYKAI	240
DB	241	IFVIMAVFEIETPVYVALLSSYOSILFNGNCEKRLKDLVMTVEYVAYSHCCMPVI	300
QY	241	IFVIMAVFEIETPVYVALLSSYOSILFNGNCEKRLKDLVMTVEYVAYSHCCMPVI	300
DB	301	YAFVGRFRKYLRFHFHRLMLHGLYIFPLPSEKLEKRTSSVSPSTAEPLSIVF	355
QY	301	YAFVGRFRKYLRFHFHRLMLHGLYIFPLPSEKLEKRTSSVSPSTAEPLSIVF	355

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Gao, J. L.; Murphy, P. M.	J. Biol. Chem.	Cloning and differential tissue-specific expression of three mouse beta chemokine receptor-like genes, including the gene for a functional macrophage inflammatory protein-1 alpha receptor.	EMBL:U28406; NID:9881551; PID:9881552	I49341	Preliminary; translated from GB/EMBL/DBD	DNA	1-359	#label RES	359	68.18;	DB 2:	359;	240;	49;	58;	2;	2;
#cross-references	MIMD:95340546																
Query Match																	
Best Local Similarity																	
Matches																	
Db	12	VESETTPREYEMARP-CEKVRKEIGLSMLLPPLYSLVFTIGLGMMAYLLIKRKIQ															
Qy	8	VEETGTTSTY-YDVGGLCEKADRTALMAQVPLPLSYVFTVGLGVVMMILIKRRLR															
Db	71	IMNTIYFENLAISDLELFTVPPEHIVLWENNGFGHYMKMLSGFYALYSEIFITIL															
Qy	67	IMNTIYILNLAISDLELVTLPPEHIVRHNNVFGHGKLLSGYTHGLYSEIFITIL															
Db	131	LTDRIYLAIVAAVFLARVATVATITSIITWGLAGLALPEEIPHESDPSGFCSCSP															
Qy	127	LTDRIYLAIVAAVFLARVATVATITSIITWGLAGLALPEEIPHEEETLFEETCSAL															
Db	191	YPBEEDSKRFAHLRNINFGALPLLYMYICSGIITKILRCPNNKKHAIPLIVMA															
Qy	187	YPBEYTVSWRFHFLRMTIFCLVPLPLVMAICYTGIIKTLRCPSKKKYKAIFIVMA															
Db	251	VFFIFMTPYNVLVLSFASFSTFLETSCEOSKHDLAMQVTEVATYHCCVNPYAFVGE															
Qy	247	VFFIFMTPYNVAIILSSYQSLIFGNCDESKHDLVMAVTEVATYHSCCMNPYAFVGE															
Db	311	RRKRLRLEFHRNVQFTMENIFQLPGEENGRTSSVSPSTGEODISVVF															
Qy	307	RRKRYLRHFFRHLMLGRYIPLPSEKLERISSVSPSTAEPELSIVF															
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TITLE	chemokine (C-C) receptor 1 - human																
ALTERNATE_NAMES	C-C CR-1; macrophage inflammatory protein-1-alpha receptor																
ORGANISM	formal_name Homo sapiens #common_name man																
DATE	30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 10-Sep-1997																
ACCESSIONS	A45177; I5671																
REFERENCE	A45177																
#authors	Necse, K.; DiGregorio, D.; Mak, J. Y.; Horuk, R.; Schall, T. J.																
#journal	Cell (1993) 72:415-425																
#title	Molecular cloning, functional expression, and signaling characteristics of a C-C chemokine receptor.																
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#accession	A45177																
##status	nucleic acid sequence not shown																
##molecule-type	mRNA																
##residues	1-355	#label NEO															
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REFERENCE	I5671																
#authors	Gao, J.																
#journal	J. Exp. Med. (1993) 177:1421-1427																

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Qy	1	MTSLDPLVEFTTGSYSD-DVGLLCEADPRLAAQVPLPLSLVTFVGLGNVVMIL	59	
Db	60	MOHRLQSMSTLYLFENLAVSDPLFLFPWIDYKLDKDMIFGAMCKLSGFYYGLGS	119	
Qy	60	IKYRLRLMTIYLLNLNAISDLFLVLPENIHVRGHNHVFSGMKLLSGFYHTLGS	119	
Db	120	EIFFILLITIDRYLAIVAAVAFALRARTVTGLIITSITMALAILASMPALYFFKAQMEFT	179	
Qy	120	EIFFILLITIDRYLAIVAAVAFALRARTVTGLIITSITMALAILASMPALYFFKAQMEFT	179	
Db	180	HRTSGPHEPPYKSLQMKRFQALAKNLGLIPLLVMTICTAGITRILLRPSKKVAAVR	239	
Qy	180	ETLCSALPEDVTYVSMRFHTLRATIFCLVPLLVMAICYGIIKTLRCPKSKRYAIR	239	
Db	240	LIFPITLLEFLMTVPYNLSVSVSAFOVLVFNOCOSKHLDIAMQVEVATYATHCNPI	299	
Qy	240	LIFVIMAVFFLFMTPIVAILLSYQSILRGNDESKHDLVMLTVEVLYSHCCNMPV	299	
Db	300	IYVVEGERFMKYLKQLFQHRVAIPLAKWLPISVDOLERTSSISPSGHELSAGF	355	
Qy	300	IYAFVGEFRKRYLHFFHRHLMHGRIPFLPSEKLEBRSSVSPSAPELSIVF	355	
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TITLE			#formal name Homo sapiens #common name man	
ORGANISM			21-Dec-1990 #sequence revision 06-Jun-1997 #text_change	
DATE			06-Jun-1997	
ACCESSIONS		G02653		
REFERENCE		H01541		
#authors		Combiadere, C.		
#submission		submitted to the EMBL Data Library, May 1996		
#accession		G02653		
#status		preliminary; translated from GB/EMBL/DBJ		
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#residues		1-352 #label COM		
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Db	20	COKINVKQIAARLRLPRLSLVFLIGFPGNMMLVILLINCKRLKSMITDIYLLNLAISDLFF	79	
Qy	24	CEKATRALMAQPEPLSLVTFGLGNVVMILIKYRLRLMTIYLLNLNAISDLFF	83	
Db	80	LLTVFMAHYLAAQ-WDQGNMCOULTGLYFIFGFSGIFITLTIDRYLAIVAAVAFALR	138	
Qy	84	LVTLFPMYHHYRGHNMVYGHGCKLLSGFYHTGLXSELFIITLTIDRYLAIVAAVAFALR	143	
Db	139	ARTVTEGVTIVTVVAVAFASLPDGIIFTRSQKGLNHT-CSSHFPYSQ-YQFKNFQTL	196	
Qy	144	ARTVTEGVTIVTVVAVAFASLPDGIIFTRSQKGLNHT-CSSHFPYSQ-YQFKNFQTL	196	
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Qy	202	KRTTICVLPPLLVMAICTYGIITKTLRLPS-KKRYKALRLFVIMAVFIMFTYNAIL	260	
Db	257	INTFOE-FGLNCCSSRLDOAQOVTELTMTCCIPDIYAFVGEKRYNLLVLFQKH	315	
Qy	261	LSYSISILFG-NDCKSRKHDLVMLTVTVIAVSHCCNMPVYIYAVGEFRKRYLHFFHRH	319	
Db	316	IAKRCCKCSIFQOEAPERASSVYTRSTGEQEIYV	350	

Oy 320 LLMHLGRYIFLPSEKLEKERTSSV-SPSTAEPELSTI 353

RESULT 7

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TITLE chemokine (C-C) receptor 5 - human

ALTERNATE_NAMES C-C CKR-5

ORGANISM #formal_name Homo sapiens #common_name man

DATE 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 10-Sep-1997

ACCESSIONS A43113

REFERENCE A43113

#authors Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.

#journal Biochemistry (1996) 35:3362-3367

#title Molecular cloning and functional expression of a new human CC-chemokine receptor gene.

#accession A43113

#status preliminary

#molecule_type mRNA

#residues 1-352 #label SAM

#cross-references GB:X91492; NID:g1262810; PID:e199247; PID:g1262811

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Oy 24 CEKADTRALMAQFVPPLSLVFTVGLGNVVMILIKRIRMTNTIYLLNLAIISDLF 83

Db 80 LITVPMHAYAAQ-WDFGNMQLTGLYFTGFPSGIFITLITDRYLAHVAVPAIK 138

Oy 84 LITLPEFMTHYVGHMVMVGHGMCKLLSGFYHGLTSEIFITLITDRYLAHVAVPALR 143

Db 139 ARTVGEVATSVITWVAVFASLPGIIFIRSGEKLHT-CSSHPYQ-QQFMNFTQL 196

Oy 144 ARTVFGVITSLVGLVAVLALPEFIFETE-ELFEELCALPDEDTVS-WHFHTL 201

Db 197 KIVILGLVPLLVNVCYSGILKTLRCNKKRRRAVALFTTITVYFLFWAPNYVL 256

Oy 202 RMTICVLPLLVMAICTGIIKTLRCS-KKTKAIRLIFVIMAVFIEMTPYNAVL 260

Db 257 LNTPEEF-FGLNCCSSNRLDQAOYTELGLTCCINPIIAYVGEKRYNLVFPKH 315

Oy 261 LSSYSILFG-NDCCRSKHLDMVLTVEIAYSHCCMNPVIYAFVGERFRKYLRRHFRH 319

Db 316 IAKRFCKCSIFQEAPEPASVYTRSTGEORISV 350

320 LLMHLGRYIFLPSEKLEKERTSSV-SPSTAEPELSTI 353

RESULT 8

ENTRY S55594 #type complete

TITLE G protein-coupled receptor E1 - equine herpesvirus 2

ORGANISM #formal_name equine herpesvirus 2

DATE 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Sep-1997

ACCESSIONS S55594

REFERENCE S55594

#authors Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.

#journal J. Mol. Biol. (1995) 249:520-528

#title The DNA sequence of equine herpesvirus 2.

#accession S55594

#status preliminary; nucleic acid sequence not shown

#molecule_type DNA

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#cross-references GB:U20824; NID:g695172; PID:g695173

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Oy 17 YDDVGLCEKADTRALMAQFVPPLSLVFTVGLGNVVMILIKRIRMTNTIYLLNL 76

Db 115 AISDLFLPLVPMHAYIGMTHDWTFGISLCKLRGVCYMSLSQVFCITLITDRYLA 174

Oy 77 AISDLFLPLVPMHAYIGMTHDWTFGISLCKLRGVCYMSLSQVFCITLITDRYLA 135

Db 175 VYATVALRFRVTVGVCTWFLAGLSLPEPFHGHODNRCVQDPYPMSTNWM 234

Oy 136 VHAVPALRARTVGVITSLVGLAVLAALPEFIFETEELFETLCSALYPEDYVSW 195

Db 235 RRAHAYKIMSLIPLLVNVCYVYIIRLLRSPSKKRYAIRLIFVIMAVFVFTPY 294

Oy 196 RHFHTLRMTICVLPLLVMAICTGIIKTLRCSKKRYAIRLIFVIMAVFVFTPY 255

Db 295 NVILLSTFHAATLLNOCALSSNDMALITRTVAYVHCCINPIYAFVGEKRRHLYHF 354

Oy 256 NVAILSSYQILFGNDCERSKHDLVLTVEIAYSHCCMNPVIYAFVGERFRKYLRRH 315

Db 355 FHTVATYICKYIFPLSGD 373

Oy 316 FHRLLMHLGRYIFLPSE 334

RESULT 9

ENTRY I49340 #type complete

TITLE MIP-1 alpha receptor like-1 - mouse

ORGANISM #formal_name Mus musculus #common_name house mouse

DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 28-Feb-1997

ACCESSIONS I49340

REFERENCE I49339

#authors Gao, J.L.; Murphy, P.M.

#journal J. Biol. Chem. (1995) 270:17494-17501

#title Cloning and differential tissue-specific expression of three mouse beta chemokine receptor-like genes, including the gene for a functional macrophage inflammatory protein-1 alpha receptor.

#cross-references EMBL:U28405; NID:g881549; PID:g881550

#accession I49340

#status preliminary; translated from GB/EMBL/DBJ

#molecule_type DNA

#residues 1-356 #label RES

#cross-references EMBL:U28405; NID:g881549; PID:g881550

SUMMARY #length 356 #molecular-weight 40934 #checksum 563

Query Match 52.1%; Score 1439; DB 2; Length 356;

Best Local Similarity 52.3%; Pred. No. 2,38e-187;

Matches 174; Conservative 77; Mismatches 80; Indels 2; Gaps 2;

Db 22 GFLCPSINVARFGITVPTPLSLVFIIGVGLVVLVLIQKRLRNMTSYLFNLAISD 81

Oy 21 GLCEKADTRALMAQFVPPLSLVFTVGLGNVVMILIKRIRMTNTIYLLNLAIISD 80

Db 82 LVFLSTLPEFWDYIMKGMIRGNMCKFVSGFYLLGLXSMFEFTLITDRYLAHVAV 141

Oy 81 LFLVTLPEFMTHYVGHMVMVGHGMCKLLSGFYHGLTSEIFITLITDRYLAHVAV 140

Db 142 ALRRTVFGIISLITWVLAALVSIPLCYVF-KSQEFYHTCRALIPRSLRFLRFQ 200

Oy 141 ALRRTVFGIISLITWVLAALVSIPLCYVF-KSQEFYHTCRALIPRSLRFLRFQ 199

Db 201 ALTNMILGLPLLVNVCYRIINVLHRRNKKRKYAIRLIFVIMAVFVFTPYLAA 260

Oy 200 TLRMTICVLPLLVMAICTGIIKTLRCSKKRYAIRLIFVIMAVFVFTPYNAVL 259

Db 261 FVSAFEDVLPSPCLRSQVDLSMTBALAYTHCCVNPVYVGVGRFRKRYLMQLRRH 320

QY 260 LLSYOSILGNDGERSKHDVLVMTVEVIAVSHCCNMPVIAVFGGRFRKYLHFFHRH 319

Db 321 TAITLPQWLPFLSDRAQRASARLPSTVEIETS 353

QY 320 LLMHLGRYIPFLPSEKLERTSSVSPSTAEPELS 352

RESULT 10

ENTRY JC2443 #type complete

TITLE Chemokine (C-C) receptor 2, splice form B - human

ALTERNATE_NAMES C-C CR-2; monocyte chemoattractant protein 1 receptor; monocyte chemotactin 1 receptor

ORGANISM #formal_name Homo sapiens #common_name man

DATE 21-Feb-1995 #sequence_revision 03-Apr-1995 #text_change 10-Sep-1997

ACCESSIONS JC2443

REFERENCE JC2443 Yamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N. Biochem. Biophys. Res. Commun. (1994) 202:1156-1162

#journal Molecular cloning and functional expression of a human monocyte chemoattractant protein 1 receptor.

#accession JC2443

#molecule_type mRNA

#residues 1-360 #label YAM

REFERENCE A53477

#cross-references DBJ:D29984; NID:9531246; PID:d1006817; PID:9531247

#authors Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R. Proc. Natl. Acad. Sci. U.S.A. (1994) 91:2752-2756

#journal Molecular cloning and functional expression of two monocyte chemoattractant protein 1 receptors reveals alternate splicing of the carboxyl-terminal tails.

#cross-references M01D:94195821

#accession I38450

#molecule_type mRNA

#status preliminary

#residues 1-374 #label RES

GENETICS #cross-references EMBL:U03882; NID:9472555; PID:9472556

#gene GDB:CKKBR2

#cross-references GDB:337364; OMIM:601267

#map_position 3p21-3p21

KEYWORDS alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane protein

FEATURE

3-70 #domain transmembrane #status predicted #label TM1

61-100 #domain transmembrane #status predicted #label TM2

115-136 #domain transmembrane #status predicted #label TM3

154-178 #domain transmembrane #status predicted #label TM4

207-226 #domain transmembrane #status predicted #label TM5

244-268 #domain transmembrane #status predicted #label TM6

287-309 #domain transmembrane #status predicted #label TM7

14 #binding_site carbohydrate (Asn) (covalent) #status predicted

113-190 #disulfide_bonds #status predicted

SUMMARY #length 360 #molecular_weight 41063 #checksum 1732

Query Match 51.5%; Score 1421; DB 2; Length 360;

Best local Similarity 52.8%; Pred. No. 1,17e-184;

Matches 181; Conservative 88; Mismatches 64; Indels 10; Gaps 8;

Db 21 TTFEDYDYGAPCHKFDVKQIGAOQLPPPLYSVIFGFGVGMVLVLLINCKKLKCLTDIY 80

QY 14 TSYD-DVGLCEKADTRALMAQFVPLPSVFTVGLGNVVVMILIKRRLRMINTY 72

Db 81 LLMNLSIDLFLTLPLMAHSA-ANENVFGNACKLTGLYHIGFGGIFITILLTDIY 139

QY 73 LLMNLSIDLFLTLPLMAHSA-ANENVFGNACKLTGLYHIGFGGIFITILLTDIY 132

Db 140 LAIVHAFALKARTVTEGVTSVTIMLVAVFASVGIIFTCCKEDSVYVCGPFP--R- 196

QY 133 LAIVHAFALKARTVTEGVTSVTIMLVAVFASVGIIFTCCKEDSVYVCGPFP--R- 192

Db 197 -GNMNHHTIRNLTGLVPLLVITVICYSGILTKLLCRNEKRRHRAVRITFTIMYVFL 255

QY 193 YSWRHHTIRNLTGLVPLLVITVICYSGILTKLLCRNEKRRHRAVRITFTIMYVFL 251

Db 256 WPEYNIIVLLNTFOEP-FCGINSCESTSQLDAQOVNETGLMTHCCINPIIYVGEKFR 314

QY 252 WPEYNIIVLLNTFOEP-FCGINSCESTSQLDAQOVNETGLMTHCCINPIIYVGEKFR 310

Db 315 YLSVFFRKHTKRCQCPVREYDGVTSINTPSTGDEVS 357

QY 311 YLRHFFRHLLMHLGRYIPFLPSEKLE-RTSSVSPSTAEPELS 352

RESULT 11

ENTRY I38450

TITLE Chemokine (C-C) receptor 2, splice form A - human

ALTERNATE_NAMES C-C CR-2; monocyte chemoattractant protein 1 receptor; monocyte chemotactin 1 receptor

ORGANISM #formal_name Homo sapiens #common_name man

DATE 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 29-Aug-1997

ACCESSIONS I38450

REFERENCE A53477

#journal Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R. Proc. Natl. Acad. Sci. U.S.A. (1994) 91:2752-2756

#journal Molecular cloning and functional expression of two monocyte chemoattractant protein 1 receptors reveals alternate splicing of the carboxyl-terminal tails.

#cross-references M01D:94195821

#accession I38450

#molecule_type mRNA

#status preliminary

#residues 1-374 #label RES

GENETICS #cross-references EMBL:U03882; NID:9472555; PID:9472556

#gene GDB:CKKBR2

#cross-references GDB:337364; OMIM:601267

#map_position 3p21-3p21

KEYWORDS alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane protein

FEATURE

44-68 #domain transmembrane #status predicted #label TM1

79-99 #domain transmembrane #status predicted #label TM2

115-136 #domain transmembrane #status predicted #label TM3

154-178 #domain transmembrane #status predicted #label TM4

208-226 #domain transmembrane #status predicted #label TM5

244-265 #domain transmembrane #status predicted #label TM6

292-309 #domain transmembrane #status predicted #label TM7

14 #binding_site carbohydrate (Asn) (covalent) #status predicted

32-277,113-190 #disulfide_bonds #status predicted

SUMMARY #length 374 #molecular_weight 41914 #checksum 5414

Query Match 48.4%; Score 1335; DB 2; Length 374;

Best local Similarity 55.5%; Pred. No. 8.06e-172;

Matches 166; Conservative 73; Mismatches 51; Indels 9; Gaps 7;

Db 21 TTFEDYDYGAPCHKFDVKQIGAOQLPPPLYSVIFGFGVGMVLVLLINCKKLKCLTDIY 80

QY 14 TSYD-DVGLCEKADTRALMAQFVPLPSVFTVGLGNVVVMILIKRRLRMINTY 72

Db 81 LLMNLSIDLFLTLPLMAHSA-ANENVFGNACKLTGLYHIGFGGIFITILLTDIY 139

QY 73 LLMNLSIDLFLTLPLMAHSA-ANENVFGNACKLTGLYHIGFGGIFITILLTDIY 132

Db 140 LAIVHAFALKARTVTEGVTSVTIMLVAVFASVGIIFTCCKEDSVYVCGPFP--R- 196

QY 133 LAIVHAFALKARTVTEGVTSVTIMLVAVFASVGIIFTCCKEDSVYVCGPFP--R- 192

Db 197 -GNMNHHTIRNLTGLVPLLVITVICYSGILTKLLCRNEKRRHRAVRITFTIMYVFL 255

QY 193 YSWRHHTIRNLTGLVPLLVITVICYSGILTKLLCRNEKRRHRAVRITFTIMYVFL 251

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Db      266 WTPYVIVVLITFOFE-GLGNSCESTSLQDADQVTEHGGHCINPIIYAFAFGKRR 313
       ||||| :||||| : | :||| : ||| ||| :: :|||:|||:|||:|||||
Oy      252 WTPYVAVLLISYSQILFG-NDCERSKLDMLVMTVEYIAISHCCMPVIATFVGKKR 309

RESULT 12
ENTRY   A57160 #type complete
TITLE   chemokine (C-C) receptor 4 - human
ALTERNATE_NAMES C-C CKR-4
ORGANISM Homo sapiens #common_name man
DATE     10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change
        15-Aug-1997
ACCESSIONS A57160
REFERENCE  A57160
AUTHORS    Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf,
           A.J.; Proudfoot, A.E.L.; Wells, T.N.C.
           J. Biol. Chem. (1995) 270:19495-19500
           Molecular cloning and functional expression of a novel CC
           chemokine receptor cDNA from a human basophilic cell line
#accession A57160
#status preliminary; not compared with conceptual translation
#molecule_type mRNA
#residues 1-360 #label POW
#cirs-references GB:X85740
#note source clone K5-5
GENETICS GDB:CMKR4
#gene ##cirs-references GDB:677463
#map_position 3p21-3p21
KEYWORDS G protein-coupled receptor; glycoprotein; phosphoprotein;
          transmembrane protein

FEATURE
40-65 #domain transmembrane #status predicted #label TM1\
76-97 #domain transmembrane #status predicted #label TM2\
112-133 #domain transmembrane #status predicted #label TM3\
151-175 #domain transmembrane #status predicted #label TM4\
208-226 #domain transmembrane #status predicted #label TM5\
243-264 #domain transmembrane #status predicted #label TM6\
291-308 #domain transmembrane #status predicted #label TM7\
28-276,110-187 #disulfide_bonds #status predicted\
72,350 #binding_site phosphate (Ser) (covalent) (by casein
         kinase II) #status predicted\
145 #binding_site phosphate (Ser) (covalent) (by protein
     kinase C) #status predicted\
183,194 #binding_site carbohydrate (Asn) (covalent) #status
         predicted\
321 #binding_site phosphate (Thr) (covalent) (by protein
     kinase C) #status predicted
SUMMARY #length 360 #molecular_weight 41402 #checksum 4713
Very Match 45.0% Score 1243; DB 2; Length 360;
Best Local Similarity 45.6%; Pred. No. 4,066-158;
Matches 160; Conservative 83; Mismatches 103; Indels 5; Gaps 5

Db      9 TTLDL-SLYSNVLYESIPKCTKEGIRAFGEFLPPLSYLFVFEGLGNSVYLVEFKY 67
       ||::| :| :| :| :| :||| ||||| |||:|:|
Oy      3 TSLDIVERFTTGYDDGLCEKADRFALMAQFVPPLYSIFVTGVLGNVVMMILIKY 62

Db      68 KRLRSMDEVILLNLAISDLLEFVSLEPFMGYYAADO-WYFGIGLKRMASMTLVGFYIGIF 126
       ::|||::|:|||||:||||| : ||| :|||:| :||| ||
Oy      63 RRLRIMTYILLNLAIISDLLEFLVLPFWIHVRHNNWFFGHGMCKLLSGFHTGLYEIEIF 122

Db      127 FVMLSIDRYLAIVAVSLRARLTGVTVTSITWSVAVASDPGFSEFCYERKNHTY 186
       |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Oy      123 FIILLTDRIYLAIVAAVAPARVTVTSVITYTWGLAVLAALPEFIYTEBELFEEL 182

Db      187 CKTKYSLNST-TWKVLSLEINILGLVTLPIGLIMFCYSMIIRLOHKNEKNNAVMIF 245
       | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Oy      183 CSAIPEDPTIVSWRHFRHLRMTCICVPLPVMAICYGIKITLLRCPSKKYAIRLIIF 242

Db      246 AVVVLFGFWPPYNIIVLFLETLVELVYIQDCTFERIDYAIQAETELAHHCCNLPITFY 305
       ::::|:|||||:|:|:| :| :| :| :| :| :| :| :| :| :| :| :| :|

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QY	243	VIMAEFFETFWPYNAIILSSQSIILFGNDICERSKHDLVMTLVEVIAVSHCCNNPIYA	302
Db	306	FLGEEFKRYIIQLKRTCKGLFVLCQYCGGLQIYTSADIPSSSYOSTMDHL	356
QY	303	FVGEFRFKRYILRHFPHR-HLMLHLQRYIPFLPSEKLE-RTSSVSPSTAEP	351
RESULT	13		
ENTRY	JC4587	#type complete	
TITLE	Chemokine (C-C) receptor 4 - mouse		
ORGANISM	#formal_name Mus musculus #common_name house mouse		
DATE	08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 12-Dec-1997		
ACCESSIONS	JC4587		
REFERENCE	JC4587		
#authors	Hoogwerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C. Power, C.A.		
#journal	Biochem. Biophys. Res. Commun. (1996) 218:337-343		
#title	Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to murine and human CC CKR-4.		
#accession	JC4587		
#molecule_type	mRNA		
#residues	1-360 #label HOO		
#cross-references	EMBL:X90862; NID:g1167851; PID:e195632; PID:g1167852		
#experimental_source	thymus		
GENETICS			
#gene	CC CKR-4		
KEYWORDS	glycoprotein; phosphoprotein; receptor; thymus		
FEATURE			
2,183,194			
72,202,350	#binding_site carbohydrate (Asn) (covalent) #status predicted\		
145	#binding_site phosphate (Ser) (covalent) (by casein kinase II) #status predicted\		
321	#binding_site phosphate (Ser) (covalent) (by protein kinase C) #status predicted\		
SUMMARY	#binding_site phosphate (Thr) (covalent) (by protein kinase C) #status predicted		
	#length 360 #molecular_weight 41462 #checksum 7852		
Query Match	43.4%; Score 1199; DB 2; Length 360;		
Best Local Similarity	43.7%; Pred. No. 1,41e-151;		
Matches	150; Conservative 92; Mismatches 97; Indels 4; Gaps 4;		
Db	16	YNSYFFESMPKPKCKEIKAFGEVFLPPLYSLLVGLFGNSVNVLVLEFKYRLKSM	75
QY	11	FGTTSYDDVGLCEKADTRALMAQFPPLYSLLVGLFGNSVNVLVLEFKYRLKSM	70
Db	76	VYLLNLAISDLLFLSLPFWGYAADQ-WPFGGLCKIVSMWLVGYSIFIMLSID	134
QY	71	IYLLNLAISDLLFLVLPFWIHYRGHWVFGHCKMLLSGFYHTGYSISIFILLITD	130
Db	135	RYLAIVAHVFLSKARTLVGYVTLITWVAVFAFSLGLFTSCYTEHNHTYCKTOYSN	194
QY	131	RYLAIVAHVFLSKARTLVGYVTLITWVAVFAFSLGLFTSCYTEHNHTYCKTOYSN	190
Db	195	ST-TWVVLSSLEINVLGLLPLGLIMLFWYSMIITFLOHCKNEKNRAVMIQGVVLF	253
QY	191	TVYSWRHPTLRMTIFCLVPLPLVMAICYGIIITLDRCPKSKYKRIPLFVIMAE	250
Db	254	FWTPTNVVLELVELEVDCTLEKYLDAIDATDTLTFHICCLNPVYIFFLGKFKR	313
QY	251	FWTPTNVVLELVELEVDCTLEKYLDAIDATDTLTFHICCLNPVYIFFLGKFKR	310
Db	314	YITOLFTRCGPLVLCXKCDPLQYASDMSSSYOSTVHDF	356
QY	311	YLRHFFER-HLMLHLGRITPLPSEKLEKRTSSV-SPSTAEP	351
RESULT	14		
ENTRY	JC5067	#type complete	
TITLE	G protein-coupled receptor CKR-L1 - human		
ALTERNATE_NAMES	Chemokine receptor-like protein TER1; GPR-CY6		
ORGANISM	#formal_name Homo sapiens #common_name man		

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DATE 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change
ACCESSIONS 10-Sep-1997
JC5067; G02776; G02387
REFERENCE
#authors Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.
#journal Biochem. Biophys. Res. Commun. (1996) 227:846-853
#title Molecular cloning and RNA expression of two new human chemokine receptor-like genes.
#accession JC5067
#molecule_type DNA
#residues 1-355 #label ZAB
#cross-references EMBL:279782; NID:g1668735; PID:6264772; PID:g1668736
REFERENCE
#authors Rocchi, M.; Santoni, A.
#submission Napolitano, M.; Zingoni, A.; Bernardini, G.; Spinetti, G.; submitted to the EMBL data library, June 1996
#accession G02776
#status translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-355 #label NAP
#cross-references EMBL:062556; NID:g1468978; PID:g1468979
REFERENCE
#authors Bonner, T.I.
#submission Submitted to the EMBL Data Library, January 1996
#accession G02387
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-355 #label BON
#cross-references EMBL:045983; NID:g1245056; PID:g1245057
COMMENT This protein belongs to the family of beta chemokine receptors.
GENETICS
#gene TER1
#keywds G protein-coupled receptor; transmembrane protein
#feature
FEATURE
36-63 #domain transmembrane #status predicted #label TM1\
73-94 #domain transmembrane #status predicted #label TM2\
108-129 #domain transmembrane #status predicted #label TM3\
147-171 #domain transmembrane #status predicted #label TM4\
200-222 #domain transmembrane #status predicted #label TM5\
239-260 #domain transmembrane #status predicted #label TM6\
281-304 #domain transmembrane #status predicted #label TM7\
SUMMARY
#length 355 #molecular-weight 40844 #checksum 2562
Query Match 39.1%; Score 1067; DB 2; Length 355;
#local Similarity 39.1%; Pred. No. 5, 11e-132;
#atches 133; Conservative 96; Mismatches 103; Indels 8; Gaps 6;
Db 1 MDYTLDSVTVTDYDYPDIFSSPCDAELIQTNKRLLAFFYCLLFVSLGNSVILVL 60
OY 1 MTSLSIDVETGTSYDDV-GLCEKADPTBALMAQFPPYSLVFLVGLGNVVMIL 59
61 VVCKRLBSITDVIYLLNLASDLLEVFSPFOTYYLLDQ-VWFGVWCKVYVSGFYICFYS 119
OY 60 IKYRLRLMTIYIYLLNLASDLLELVLPFWIHVRGHVNWFGHGMCKLSGFGYTHLGS 119
Db 120 SMEFTLTSVDRYAVYAVYALVVRITRMGTICLAVWLAIVLAIWATPILVYGVASE-D 178
OY 120 EIFFILITIDRYLIAVYAVYALVVRITRVFTVTSIVTWGLAVIAALPDEIFYETELFE 179
Db 179 GVLOCSFYNOOTL-KWKIFTFNKMIILGILPTIFMFCYIKILHOLDKRQNNHTRKAI 237
OY 180 ETL-CSALYPEDYVSWMHFTLMTITFCVLPLLVMAICITGLIKLLKCPSSKKAKAI 238
Db 238 RLVLIVYASLLEWYPRVNVLFLLSLSHMTLDGCSISQQLTYATHVTEIITSHTCCVP 297
OY 239 RLFIYIAVVFIEFWYPRVNVALLTSYOSILFNGNCCESKSHDLVMTLVEVIAVSHCCMP 298
Db 298 VIYAVGEKFKHLSEIFQKSCOSQFVNTLQGMRESEK 337
OY 299 VIYAVGEKFKYLRHFTHR--HLMLHNGYKIPPLSEK 335

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RESULT#   15
ENTRY      hypothetical G-protein coupled receptor - rat
TITLE      #formal_name Rattus norvegicus #common_name Norway rat
DATE       26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
          30-May-1997
ACCESSIONS 158186
REFERENCE   158186
AUTHORS     Harrison, J.K.; Barber, C.M.; Lynch, K.R.
JOURNAL     Neurosci. Lett. (1994) 169:85-89
#title      cDNA cloning of a G-protein-coupled receptor expressed in rat
            spinal cord and brain related to chemokine receptors.
#cross-references MIMD:94323113
accession   158186
#status      preliminary; translated from GB/EMBL/DBDJ
#molecule_type mRNA
#residues    1-354 #label RES
#cross-references EMBL:U04608; NID:9439860; PID:9439861
KEYWORDS    G protein-coupled receptor
SUMMARY     #length 354 #molecular_weight 40327 #checksum 4478

Query Match           38.4% Score 1059; DB 2; Length 354;
Best Local Similarity 44.8%; Pred. No. 7.78e-131;
Matches 139; Conservative 77; Mismatches 89; Indels 5; Gaps 4.

Db 15 YDDSAEACYGLDYAFGRIFSLFISLFVTEFGVLGNLVLTATNSKRKSTDIYLLNT 74
||| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Qy 17 YDDVGILDEKMDTRALMAQFPVPPLYSLSVTFTGLGNNVVVMILIKRYRIRMTIYLNL 76

Db 75 ALSDLLFYATLPFWTHYLISSHE-GLNAMACKLTTPAFFIGFEFGIFPTIVASIDRYLAIV 133
||:||||| : |||| : : : || : : : || : : : || : : : || : : : || : : : ||
Qy 77 AISDLFLPYTLPFWTHYVRGHNVWFEGMCKLLSGEFHTGYSIEIFFILLITIDRYLAIV 136

Db 134 LAANSMMNRRTQHGGTTISLGVAAMAALLVASQPMFTFRKD--NCLT-GD-YPEVLQEIWP 169
+ : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||
Qy 137 HAVFALRRARYTVFGYVISITWGIAVLADAEPIFFETEELEETELTSALYEPDTVYSMR 196

Db 190 VLRNSEVNIILCFVPLLLMSFCYRIYATPESCKANRKARAIRLLVVVFLEMTPN 249
|| : : : ||||| : |||| : : : ||||| : |||| : : : ||||| : |||| : : : ||
Qy 197 HFHTRLRMITPCGVLPDLVMAICYGIKITLLRCPSKKRYAIRLIPYIMAVFIPTWPN 256

Db 250 IVILETLKFNPSPSCGMKRDLMWALSVTETAFAASHCCQLPFITYAAGEKFRRLYHLX 309
|| : : : || : : : || : : : || : : : || : : : || : : : || : : : || : : : ||
Qy 257 VALISSYQSILFGNDCKSRKLDLVMLYTEVIAYISHCAMPVIYAFVGERFRKLHHFE 316

Db 310 NKCLAVLCGR 319
:: : : ||
Qy 317 HRHLLMHNGR 326

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